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113 ACCCCGAGCGCCGTCCTGCCGGGCCGAGGCCGCCTTCTCTGTCTTCACGGTCCTG 172
173 GIGGIGACGCIGCIAGIGCIGCIGAICGCIGCCACITICCIGIGGAACCIGCIGGIICCG
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                                                                                                                                                                 Sequence 8, Application US/08356405
Sequence 8, Application US/08356405
Patent No. 5807691
GENERAL INFORMATION:
APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Henselve, Ursula
APPLICANT: Henselve, Jean-Luc
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for TITLE OF INVENTION: Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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Pred. No. 8.6e-94;
0; Mismatches 284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38,619
ER: EX92004-US
                                                                                                                                                                                                                                                                                                                                                                                               Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTY NOTICE OF THE PATENTY NOTICE OF T
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Rhone-Poulenc Rorer
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (610) 454-3839
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ilarity 70.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1073 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (610)454-3808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, Julie K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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US-08-356-405-8
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Matches
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              CCATGGAGGCCGTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACCCG
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                  682709 segs, 277475446 residues
                                                                     OM nucleic - nucleic search, using sw model
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1152
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Sequence:
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5: /cgn2_6/ptcdata/2/ina/PCTUS COMB.seg:*
6: /cgn2_6/ptcdata/2/ina/Ackfiles1.seg:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued_Patents_NA:* seq length: 0 seq length: 2000000000 Minimum DB e Maximum DB e Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	-	Semience 1, Appli	,	, ,	equence 10		Semience 1197 An	equence 15.	, r	Semience 629 Ann	equence 24		٠,		ה	מי		Seguence 3, Appli	equence 3,	Segmence 3. Appli	emience 3	equence 14	equence 2	, (denter o'	o due to de	equence 1,
	, en	-031-5	-08-356-405	-08-356-405-	1-538-	6-434-	6-434-10	US-09-016-434-1197	US-08-475-742-15	-293-1	-594-6	US-08-722-001-24	-08-351-473B	US-08-334-698-3	-08-228-932-	-08-468-939-	38-406-R55A	-08-722-190-	8-244-354-	9	US-09-444-783-3	US-09-688-415-3	US-09-016-434-1402	-783-3	042	-60	-772A	-916
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1270	3683	3683	1579	1987	1997	2004	1639	1639	1639	1630	100	1639	1639	1639	1639	1630	CC07	1639	1639
7.7	7.7	7.7	7.4	7.3	7.3	7.3	7.2	7.2	7.2	7	• •	7.7	7.2	7.2	7.2	7 2		7.2	7.2
88.2	88.2	88.2	85.6	84.6	84.6	84.6	83	83	83	83	0 6	0	83	83	83	83	9 6	83	83
28	59	30	31	32	33	34	35	36	37	800	0 0	J .	40	41	42	43		44	45

ALIGNMENTS

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Length 2226;
                                                                                                                                                                                  DNA ENCODING
               GENERAL INC. 5968817
GENERAL INFORMATION:
APPLICANT: Sticliffe, J Gregor
APPLICANT: Exlander, Mark G
APPLICANT: Lovenberg, Tinchy W
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
INTERED OF INVENTION: THE RECEPTORS, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.4%; Score 729.8; DB 2; 79.6%; Pred. No. 1.3e-145; ive 0; Mismatches 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRS:
TELECOMMUNICATION INFORMATION:
TELEFROM 619-554-2937
TELEFRAX: 619-554-2937
TELEFRAX: 619-554-2937
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2226 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 79.6
Matches 911; Conservative
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HYPOTHETICAL: 1
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US-08-031-538-1
                                                                                                                                                                                                                                                                                                                                                                                           92037
RESULT 1
US-08-031-538-1
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Gaps

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Indels

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pick's disease, Huntington's disease, Parkinson's disease, hypertension, atherosclerosis, myocardial infarction, gastritis, cirrhosis, cytostatic, osteoporosis, Crohn's disease, acquired immunodeficiency syndrome, AIDS, anaemia, asthma; rheumatoid arthritis, diabetes; obesity, drug screening, transgenic animal, allergy, gene therapy, hepatotropic, anticonvulsant, nootropic, neuroprotective, cardiant, immunosuppressive; anorectic; virucide; receptor.

Homo sapiens

/note= "Transmembrane domain" 66. 370 /label= Human_mature_GCREC-15 /note= "Transmembrane domain" 1. .65 /label= Signal_peptide Location/Qualifiers . 316 .68 Peptide Protein Domain Domain

07-FEB-2002

2000US-0223268P. 2000US-0227054P. 2000US-0231121P. 2000US-0232243P. 2000US-0232691P. 2000US-0235146P. 25-JUL-2001; 2001WO-US023433 03-AUG-2000; 21-AUG-2000; 08-SEP-2000; 13-SEP-2000; 22-SEP-2000;

(INCY-) INCYTE GENOMICS INC.

Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR; Bliot VS, Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA; Yao MG, Lu Y, Triboulay CM, Policky JL, Kearney L, Graul RC; Warren BA, Lee EA, Ding L;

WPI; 2002-188744/24. N-PSDB; AAD29681. New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic disorders

Claim 1; Page 133-134; 150pp; English.

The invention relates to novel human G-protein coupled receptors (GCREC) and their encoding polynucleotides. GCREC is useful as an immunogen for preparing monochonal and polyclonal antibodies. GCREC is useful for diagnosing, treating and perventing a cell proliferative disorder (e.g., epilepsy, classase, provided and social disorder (e.g., epilepsy, populatis, psoriasis, cancer), a neurological disorder (e.g., epilepsy, classase), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, clarrosis, cornel and fasease), an autoimmune/ inflammatory disorder (e.g., cirrhosis, anthonic an autoimmune/ inflammatory disorder (e.g., diabetes, obesity, categorosis), and viral infections. GCREC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene creating differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as thybridization probes for mapping naturally occurring genomic sequences. GCREC is useful in Southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbant (ELISA)-like assays, and in

88868	microarra GCREC exp Sequence	ys utili ression. 370 AA;	sing fluids or The present se	tissues from pati equence is human (tients to detect altered GCRBC-15
Align Pred. Score Percel Best J Query DB:	nent Sco No.: it Simil Local Si Match:	res: arity: milarity:	1.86e-136 1861.50 97.63% 97.63% 86.42%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	370 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
US-0	9-976-782	-15 (1-11	52) x AAE18654	(1-370)	
ζ	ស	ATGGAGGC	GCTAGCCTTTCAG	CACCGCCGGCGT	CTGGGACCCGAG 6
qq	н	MetGluAl	euSerV	lAlaThrAlaGlyVa	laLeuAlaLeuGlyProGl
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λŏ	125	Eccencer	ccepece	decerricierer	CACGGTCCTGGTGGTGACGC
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δ	305	GAACTAGT	GCAGCGCTGGCGA	CACCGAGCCTGGC	SAGTGAGCTGTCGACC
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δ	425	CTGTGCTG		BACGTGGCGCCAT	CCGCGACGGGGC 4
QQ	136	LeuCysCy	roAlaGlyLe	yAsnvalAlaAlaIl	AlaLeuGlyArgAspGlyAl
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λŏ	545	GCGCTCGC	зестессетсев	SCTCATCGCCCTCGC	CGCTGCTTTTGGCCGGGG
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δλ	0	GAGGTGTG	GACGCTCGGCTCC	GCGCTGCCAGGTGA	GGGGAACCCTCTATGCCGCC 6
qq	196	GluValCy	aArgLeuG]	nArgCysGlnVal	ArgGluProSerTyrAlaAl
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The present invention provides the protein and coding sequences pf novel human G-protein coupled receptors, designated NOVI, NOV2, NOV3, NOV4, NOV5a, NOV5b, NOV5b, NOV5b, NOV5b, NOV5b, NOV5b, NOV7, NOV8b, NOV8b, NOV9b, 
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           G protein-coupled receptor related polypeptides and polynucleotides diagnosis, prevention and treatment of metabolic, neurodegenerative, inal, immune, hematopoietic disorders, diabetes, obesity and
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Patturajan M, Gusev
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N-PSDB; ABA01984.
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Shimkets RA,
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immune disorder; haematopoietic disorder; developmental disease; cancer; retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; psychotic disorder; G-protein coupled receptor; cytostatic; antidiabetic; virucide; neuroprotective; nootropic; analgesic; antidepressant; antimigraine; anticonvulsant; neuroleptic; antidispermatic; antialinflammatory; anorectic; antiarthritic; antipsorlant; antiarberosclerotic; antibacterial; fungicide; osteopathic; protozoacide; antiulcer; hypertensive; hypotensive; antimifertility; vulnerary; nephrotropic; antilipemic;
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                                                                                               Human; NOV5b; metabolic disorder; neurodegenerative disorder;
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Patturajan M, Gusev
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Liu X, P
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24. .1136
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/product= "NOV5b"
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Shimkets RA,
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29-MAR-2001;
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New G protein-coupled receptor related polypeptides and polymucleotides for diagnosis, prevention and treatment of metabolic, neurodegenerative, retinal, immune, hematopoietic disorders, diabetes, obesity and

2001-626379/72.

P-PSDB; AAM47212

The present invention provides the protein and coding sequences of novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV4,

Claim 8; Page 46; 194pp; English

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NOV5a, NOV5b, NOV6a, NOV6b, NOV7, NOV8a, NOV8b, NOV9 and NOV10. These can be used in the treatment of NOVX related diseases, including cancer, metabolic, neurodegenerative, immune, haematopoietic, developmental, retinal, feeding, neurological and psychotic diseases and disorders and infections. The present sequence is the NOV5b coding sequence, the gene for which is found on chromosome 2. The NOV5b protein shares homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1150;
                                                                                                                                                                                                                                                                                                                                                    Sequence 1150 BP; 178 A; 388 C; 355 G; 229 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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Pred. No. 5.6e-221;
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ajan M, Gusev VY;
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Pred. No. 1.1e-221;
0; Mismatches 0; Indels 27
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                                                                                                    Location/Qualifiers
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serotonin receptor; chromosome 2;
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Best Local Similarity 97.7%;
Matches 1125; Conservative
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14-APR-2000;
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Sequence 1, Application US/08356405 Patent No. 5807691 GENERAL INFORMATION:

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APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Hen, Rene
APPLICANT: Han, Rene
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for These
TITLE OF INVENTION: Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650 GGCTITCTAGCTGCGGCCACATTCACTTGGAACCTGCTGGTGCTGGCTACCATCCTCAAG
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COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
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Pred. No. 4.1e-81;
0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, Julie K
REGISTRATION NUMBER: 38,619
REFERNCE/DOCKET NUMBER: EX92004-US
TELECOMMINICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
                                                                                                                                                                                                                    SEE: Rhone-Poulenc Rorer Inc.: 500 Arcola Road, 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 67.3%;
Matches 684; Conservative
                                                                                                                                                                                                                                                                                                                                      ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION:
US-08-356-405-1
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STATE:
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                                                                                                                                                                                                                                            34,163
R: TSR5099P
                                      US/08/031,538
                                                                                                                                                                                                     NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TE
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 619-554-6317
TELEPAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2155 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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hes 663; Conservative
CURRENT APPLICATION DATA:
                                                                             19930315
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APPLICANT: Elander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA I
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
ONRESPONDENCE: 73
CORRESPONDENCE ADDRESS:
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COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
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                                                                    103 ceredadaerrecradadecedecedecedecederarrecedadecedecederaderade
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                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGT 353
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                                                                                                                                                 TGGTGACGCTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGG
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Sequence 1077, Application US/09016434

Sequence 1077, Application US/09016434

Sequence 1077, Application US/09016434

Sequence 1077, Application US/09016434

APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

INTER OF INVENTION: PATHWAY GENE EXPRESSION

CORRESPONDENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
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                                                                 GCCCACTCTGTGCCTGCAGCCTGCCCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGCT 1052
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                                                                                                                                             992
GAATICTGATTGGCGTGTTTGTGCTGCTGGATCCCCTTCTTCCTGACGGAACTCATCA
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 104.4; DB 4;
Pred. No. 2e-13;
0; Mismatches 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1256 Application US/09016434

Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1113 CCTTCAAGAGCCTCTTTACTAAGCAGAGATGA 1144
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-O
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1256:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.4%;
Matches 313; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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CLASSIFICATION:
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US-09-016-434-1256
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LIBRARY: GENBA
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1417 ccarcarcraccacrarrargaggacracaggacraggagagaggaggaggriccracar 1476
                                                                                             1180 AGGIGCCCAGGACCCCACGCCCAGGGTGGAGICTGCTGACAGCAGGCGTCTAGCCACGA 1239
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834 AAGIGGIGITICACGGCACATIGCAAAGCAACGGIGICCTICCAGGIGAGCGGGGACTCCT 893
                                                                                                                                                                                                                                                                                  1240 AddacaGCAGGAAGGCCCTGAAGGCCAGCCTGACGTGGGCATCTGGGCATGTTCT
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Ratent No. 6500338

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jaffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAX GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PA-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/016,434
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1490
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STRANDEDNESS: single
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FILING DATE: HEREWI
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; CLONE: 9181431
US-09-016-434-1197
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Pred. No. 1.9e-11;
0; Mismatches 513; Indels
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                                                                                                                                                                                                    NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERNCE/DOCKET NUMBER: 97,001
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 845-0166
INFORMATION FOR SEQ ID NO: 1077:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.1%;
Matches 489; Conservative
                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Zeller, Karen J.
                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE:
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; CLONE: 91162923
US-09-016-434-1077
                                                                    FILING DATE:
CLASSIFICATION:
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LOCATION: 1...2428
OTHER INFORMATION: /note= "Rat d2 receptor sequence"
PUBLICATION INFORMATION:
                                                                                                                                                          Sequence 15, Application US/08261293
Patent No. 6486310
CENERAL INFORMATION
CENERAL INFORMATION:
CAPPLICANT: Todd, Richard D.
TITLE OF INVENTION: Receptor
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachstree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Christie, M.
Machida, C. A.
Neve, K. A.
Civelli, O.
Cloning and expression of a rat D2 dopamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; RELEVANT RESIDUES IN SEQ ID NO: 15: FROM 1 TO 2428 US-08-261-293-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/261,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6524
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Rattus norvegicus
TISSUE TYPE: Cardiac Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bunzow, J. R.
Van Tol, H. H.M.
Grandy, D. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2428 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           783-787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1988
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                                                                                                                                  US-08-261-293-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
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                                                                                                     RESULT 9
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                                                                                                                                                                                                                                                                           1019
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                                                                                                                                                                                                                                                                                                                                                                                                         1550 circiccióracadececricacórdecidaderárorcaacaececergaacecerar 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1020 CCATCTGGAAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTTCAACCCCCTGA 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1241 CAGTCCTCTACAGGGCCTTCACATGGGGGCTATGTCAACAGTGCCGTCAACCCCATCA 1300
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                                                                                                                                                                                                                                                                       960 GCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1121 AGCAGAAGGAGAAGAAAGCCACTCAGATGCTTGCCATTGTTCTCGGTGTTCATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960 GCTGGATCCCCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCC
                                                                                                                                     900 AGCAGAAGGAGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGT
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                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08475742

Patent No. 6121015

GENERAL INFORMATION:
APPLICANT: 0'Malley, Karen L
APPLICANT: 0'Malley, Karen L
APPLICANT: 0'Malley, Karen L
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REPRENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,742

CURRENT FILING DATE: 1995-06-07

EARLIER APPLICATION NUMBER: US 08/261,293

EARLIER APPLICATION NUMBER: US 08/261,293

EARLIER APPLICATION NUMBER: US 08/261,293

EARLIER PILING DATE: 1993-01-28

NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1610 TCTACACCACCTTCAACATTGAGTTCCGCAAGGCCTTCCTGAAGATCCTT 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1080 TITACACAGCITITAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTT 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080 TTTACACAGCTTTTAACAAGAACTACAACAAGCCTTCAAGAGCCTCTT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
   Length 1756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: Cloning and expression of a rat D2 dopamine receptor IITLE: cDNA.
Score 94; DB 4; Length 175
Pred. No. 3.4e-11;
0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.1%; Score 93; DB 3; Length 242
Best Local Similarity 62.9%; Pred. No. 5.8e-11;
Matches 144; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)..(2438)
OTHER INFORMATION: Rat d2 receptor sequence
PUBLICATION INFORMATION:
Query Match
Best Local Similarity 63.0%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 2428
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; VOLUME: 336
; PAGES: 783-787
; DATE: 1988
US-08-475-742-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: CDNA
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCTCCATCGGGCCTCTCCTTGGGTGGAAGGAGCCGGCACCCAACGAT---GACAAGGA 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 CTTCTGTGACATCTGGGCAGCCGTGGATGTCCTGTGCTGCACAGCGTCCATTCTGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCGCCCTCGCGCCGCTGCTCTTTGGCCGGGGGGGGGTGTGCGACGCTCGGCTCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGGCCATCGCCCTGGGCCGCGA---CGGGGCCATCACACGCCCCTGCAGCACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 Graceccarctarcarcearcearcearceaecacaractercracactarceaecacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTCACCCGGAGGAAGGCCATCTTGGCCCTGCTC---AGTGTCTGGGTCTTGTCCACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                       TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 91.2; DB 1;
Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC CODS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                         New Jersey
United States of America
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMOUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEPAX: (000) 504-3462
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/229,276
              Nerenberg, Jennie B.
Lee, Hee-Yoon
Bell, Ian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                   ADDRESSEE: Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,087
                                                                                                                                                      126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 138825
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/22
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Appollina, Mary A. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LECCHANE: (906, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
Huff, Joel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                        CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucle:
STRANDEDNESS
                                                                                                                                                                                                             COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 383;
                                  APPLICANT:
APPLICANT:
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT PILING DATE: 2001-10-12
PRIOR PAPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 629
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                  Score 93; DB 4; Length 2428; Pred. No. 5.8e-11;
                                                         85; Indels
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                                                         0; Mismatches
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US-08-722-001-24
; Sequence 24, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
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             MOLECULE TYPE: DNA (genomic)
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460; Conservative
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US-08-351-473B-7
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                                                                                                                                                                                                                                          946 CTCTACCGCTTGGCTCCTTGTTCTCCACCCTGAAGCCCCCGACGCCGTGTTCAAGGTGG 1005
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811 AAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTC
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                                                                                                                                                                                     886 CTAAGACGTTGGGCATTGTGGTCGGTATGTTCATCTTGTGCTGGCTACCCTTCTTCATCG
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                                                                      768 ---AGGATCCATTCCAAGAACTTTCACGAGGACACCCTTAGCAGTACCAAGGCCAAGGCC
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APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PH.OR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
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IBM PC compatible
3YSTEM: PC-DOS/MS-DOS
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ATTORNEY/ACENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
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COMPUTER READABLE FORM:
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APPLICANT: KAPOOR, AR
TITLE OF INVENTION: B
NUMBER OF SEQUENCES:
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US-08-351-473B-7
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           Length 1227;
Score 89.8; DB 1; Length 1 Pred. No. 2.4e-10; 0; Mismatches 442; Indels
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984 AACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCC---CATCTGGAAAAGCATATTTC 1040
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                                               694 GCTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTCGG 753
                                                                                                                                                                                                                                814 GGAAGCACCTGATGAGGCTGAAGTGGTGTTTCACGGCACATTGCAAAGCAACGGTGTCCTT 873
708 CGGGGTCACCGGAAGAACCCTTCTATGCCCTCTTCTCCTCTCTGGGCTCCTTCTACATCCC 767
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                                                                                                                                                                                                                                                                                                                      874 CCAGGTGAGCGGGGACTCCTGGCG------GGAGCAGAAGGAGAGGCGAGCCA 923
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APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-IC SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                          768 TCTGGCGGTCATTCTAGTCATGTACTGCCGTGTCTATATAGTGGCCAAGAGAACCACCAA
                                                                                                                                        754 CCGCCGCCGGAGAGCTGTGCTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1184 AGTICAAGCGCGCTTTCGTGCGCATCCT 1211
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13-APR-1994
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,933
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
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NAME: White, John P.
REGISTRATION NUMBER: 28,6
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LENGTH: 1738 base pairs
TYPE: nucleic acid
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US-08-228-932-3
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                                                                                                         APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 88.8; DB 1;
Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTOMNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37690
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 877-9550
TELEFAX: (212) 664-0525
TELEFAX: (212) 4225-23 COOP UI
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                           Sequence 3, Application US/08334698
Patent No. 5556753
                                                                                                                                                                                                                       ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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nucleic acid
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Best Local Similarity 48.9
Matches 366; Conservative
                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Best Local Similarity 48.9
Matches 366; Conservative
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US-08-468-939-3
                                                                                                                                                                                                                                                                                                                               CITY: New York STATE: New York COUNTRY: U.S.A.
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HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 7.7%; Score 88.8; DB 1; Length 1 Best Local Similarity 48.9%; Pred. No. 4.2e-10; Matches 366; Conservative 0; Mismatches 362; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101 ACTACAACAATGCCTTCAAGAGCCTCTT 1128
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US-08-468-939-3
; Sequence 3, Application US/08468939
; Patent No. 5714381
; GENERAL INFORMATION:
                                                                                                  DNA (genomic)
              single
                                                                                                                                                                                                                                                                                                                 LOCATION: 124.1683

CTHER INFORMATION:

US-08-228-932-3
                                                        unknown
                                                                                              MOLECULE TYPE: D
HYPOTHETICAL: N
STRANDEDNESS:
                                                                                                                                                                                       Z
                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                NAME/KEY:
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453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCCTCGCCCCCTCCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGCGCTG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694 GCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTCGG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           828 GAACCTAGAGGCAGGAGTCATGAAGGAGATGTCCAACTCCCAAGGAGCTGACCCTG---A 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGCGCCAICTCCAICGAICGCIACAICGGGGIGCGCIACICICTGCAGTAICCCACGCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754 CCGCCGCCGGAGGCTGTGCTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%; Score 88.8; DB 1; Length 1738;
48.9%; Pred. No. 4.2e-10;
Live 0; Mismatches 362; Indels 20
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/468,939
                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 4133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
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73	43	
ω	9	
814 GGAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTT 873	884 GGAICCATICCAAGAACITITCACGAGACACCCTITAGCAGIACCAAGGCCAAGGGCCACA 943	
814	884	
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874	874 CCAGGTGAGCGGGGACTCCTGGCGGGAGCAGAAGAAGGAGGCAGCCA 923	GCCA 923
944	944 ACCCCAGGAGIICCAIAGCIGICAAACIIIIIAAGIICICCCAGGAAAAGAAAG	 GCTA 1003

⁹²⁴ TGAIGGIGGAAIITCTGAIIIGGCGIGITITGIGCIGGIGGGGAICCCCTICITCCTGAGG 983
1004 AGACGIIGGGGAIIGIGGIGGIGGIGGIGGCIGGCIACCCIICIICAICGCIC 1063

qq

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⁹⁸⁴ AACTCATCAGCCCACTCTGTGCCTGCCTGCCCCC---CATCTGGAAAAGCATATTTC 1040 1064 PACCGCTTGGCTCCTTGTTCTCCACCCTGAAGCCCCCGACGCCGTGTTCAAGGTGGTGT 1123

¹¹⁰¹ ACTACAACAATGCCTTCAAGAGCCTCTT 1128

¹¹⁸⁴ AGTTCAAGCGCGCTTTCGTGCGCATCCT 1211

Search completed: September 7, 2004, 17:15:10 Job time : 114 secs

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5; Search time 494 Seconds (without alignments) 9906.729 Million cell updates/sec
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1 cgccatggaggccgctagcc.....aagcagagatgaacacaggg 1152
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                        7, 2004, 14:14:05
                                                                      using sw model
                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 1.0
                                                                                                                                                                            US-09-976-782-15
                                                                      - nucleic search,
                                                                                                                                                                                                                                                 IDENTITY NUC
                                                                                                        September
                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                   Scoring table:
                                                                      OM nucleic
                                                                                                                                                                                                                  Sequence:
                                                                                                        Run on:
                                                                                                                                                                            Title:
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6747726 Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100% Geneseq 29Jan04: z Database

geneseqn2003bs:*geneseqn2003cs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2004s:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abn86917 Human NOV Aba01984 Human NOV Aad29681 Human G-P Aad2963 Human G-P AbK71923 Human G-P AbK71923 Human G-D Adc86156 Human GPC Aas98053 Human GPC Murine se Mouse 5-H Rat MR22 Human 5-H Human 5-h Oligonucl Mouse 5-H Murine 5H Human 5HT Oligonucl Primary r Human 5-h Human DNA Human cDN Non-endog Description Aas98145 | Abk50434 | Abz42828 | Aad58496 Abk34848 Abi97963 Aaq56309 Abq43624 Abq43626 Abk13748 Aaq70264 Aad48747 Aaq72270 Adb52419 SUMMARIES ABK50434 ABZ42828 AAD58496 ABK71923 ADC86156 AB197963 AAQ56309 ABQ43624 ABQ43625 ABK13748 AAQ56308 AAS98053 AAQ70264 ABA01985 AAD29681 ABN86917 AAD24963 ADB52419 AAS98145 ABK34848 AAD48747 DB Length 1458 1119 11155 3086 977 2036 2061 2226 1090 1159 2700 1074 1074 Query Match 922.4 922.4 44.2 922.3 653.6 63.6 63.6 63.6 63.6 63.6 1064.8 1064 1060 Score 1016 756.2 745 732.8 732.8 729.8 729.8 721.2 497.6 497.6 37.6 496 484.4 435.2 435.2 424.6 421.4 492.B Result No. υ

	Abq43623 Oligonucl		Aah42175 Nucleotid	Aaq70265 Human ser	Aas98116 Human DNA	Aac71992 Single nu	Aac71995 Single nu	_	Abk50432 Human 5-h	Abz81690 Human LP3	Aah42174 Nucleotid		Abz81689 Polynucle	Abk50433 Human 5-h	Aad48749 Targettin	Aat88392 Corn barn	Abz42625 Human alp	Aaq64890 Human der	Abz35643 Human gen	Aca56658 Human sig	Aai99933 Human alp
AAQ72269	ABQ43623	ABQ43622	AAH42175	AAQ70265	AAS98116	AAC71992	AAC71995	AAC71989	ABK50432	ABZ81690	AAH42174	ABZ81688	ABZ81689	ABK50433	AAD48749	AAT88392	ABZ42625	AAQ64890	ABZ35643	ACA56658	AA199933
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2155	1112	1112	636	336	419	796	196	196	2543	354	297	273	225	1929	200	1140	2826	1382	1382	1382	1371
36.1	33.9	33.9	32.8	29.0	28.5	27.8	27.7	27.7	27.6	27.0	25.8	22.5	18.4	17.7	12.4	10.9	9.5	9.1	9.1	9.1	8.9
416	390.2	390.2	378.2	334.4	327.8	320	319.6	319.6	318.4	311.4	297	259.4	211.4	203.6	142.4	125.4	106	104.4	104.4	104.4	102.8
24	c 25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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antidiabetic, immunosuppressive; neuroprotective; gene therapy, cancer; cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohn's disease; multiple sclerosis; Graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                       Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
                                                                                                                                                                                                                                                                          Human NOV5 encoding cDNA sequence SEQ ID NO:15.
                                    BP
                                ABN86917 standard; cDNA; 1152
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome 2; gene; ss
                                                                                                                                                                                            29-JUL-2002
                                                                                                                  ABN86917;
ABN86917
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Homo sapiens

/*tag= a /product= "NOV5" /note= "Serotonin receptor-like protein" Location/Qualifiers 5. .1144 12-OCT-2000; 2000US-0240113P.
16-OCT-2000; 2000US-0240625P.
16-OCT-2000; 2000US-0240648P.
16-OCT-2000; 2000US-0240664P.
16-OCT-2000; 2000US-0240669P.
16-OCT-2000; 2000US-024073P.
16-OCT-2000; 2000US-024073P.
16-OCT-2000; 2000US-024073P.
16-OCT-2000; 2000US-024073P.
16-OCT-2000; 2000US-024190P. 12-OCT-2001; 2001WO-US031922 WO200230974-A2 18-APR-2002

CURAGEN CORP. (CURA-) (MILL/)

Aaq56308

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The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOV24 dare keratin 4-like protein; NOV35 is a collagen-like protein; NOV4 is a cystatin B-like protein; NOV8 is a centonin receptor-like protein; NOV65 vare cold inducible glycoprotein 30-like protein; NOV9 is a matrilin-2-like protein; NOV9 is a leukocyte surface antigen (CD53)-like protein; and cold inducible glycoprotein 30-like protein; NOV9 is a tyrosine kinase-like protein; NOV9 is a tyrosine kinase-like protein; NOV9 is a percentic, cardiovascular, antidiabetic, immunosuppressive and conting contective activities, and can be used in gene therapy. The NOVX sequences can be used in therapeutics, particularly for treating, sequences can be used in therapeutics, particularly a human. These disorders include cardiomyopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX predisposition to a disease associated with altered levels of NOVX predisposition in their papeutic or prophylactic applications for coll particularly encorer. The NOVX sequences are negotated in the treatment of feature in the presence of the particularly cancer. The NOVX sequences are negotated in the presence of or coll particularly and the treatment of feature in the presence of the particularly and in the presence of the particularly cancer. The NOVX sequences are necessarially useful in therapeutic or prophylactic applications for the presence of the particular in the presence of the particular and in the particular and the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft versus host disease. The present sequence encodes the human NOV5 protein from the present invention. NOV5 is located to chromosome 2
Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
Li L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
                                                                                                                                                                                                                                                        New NOVX polypeptides and polynucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis, cancer or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 46; 227pp; English.
                                                                                                                                                  WPI; 2002-444172/47.
P-PSDB; ABB78809.
Grosse WM,
Kekuda R, I
Edinger S,
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0 120 120 180 180 240 240 300 300 GGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGG 360 GGACGAACTAGTGGCAGCGCTGGCGATGCCACCCAGCCTGGCGAGTGAGCTGTCGACCGG 360 420 420 09 09 1 ceccarecageccecrascerricagrescacceccececerrecerrecerresere ceacaccaccaccacccccaacccccaaccccaacacaaaacrcccaac CGGCGCCGTCCTGCCGGGCCGAGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGAC ceececcercereceeeceaeecceccrrerererereaceerereseae GCTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGGAACCTGCTGGTTCCGGTCACCAT CCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTC GCGACGTCGGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGC GCGACGTCGGCTGCTGGGCCCGGAGCCTGTGCCACGTGTGGGATCTCCTTCGACGCCGGAGC 1 CGCCATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGCGCGTTGCCCTTGCCCTGGGACC CGAGACCAGCAGCGGACCCGGGGACCCCGAGAGGGGATACTCGGTTCGACCCCGAG 181 GCTGCTAGTGCTGCTGCTGCCACTTTCCTGGAACCTGCTGGTTCCGGTCACCAT ccceceeerccerecriccaccecereccecaraacrigereccrceaceecerer Gaps ; Length 1152; Indels 100.0%; Score 1152; DB 6; 100.0%; Pred. No. 7.4e-240; iive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 1152; Conservative 121 361 19 241 241 301 301 361 61 121 181

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Sequence 1152 BP; 176 A; 388 C; 359 G; 229 T; 0 U; 0 Other;

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                                                                                                          TTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; G-protein coupled receptor; GCREC-15; cell proliferative disorder; neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory; metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease; pick's disease; Huntington's disease; Parkinson's disease; hypertension; atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS; anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant; nootropic; neuroprotective; cardiant; immunosuppressive; anorectic;
               GCAGAAGGAGGGGGGGGGGCGAGGAGGAGGGGGAATTCTGATTGGCGGTGTTTGTGCTGTG 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA;
                                                                     CTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCGCCTGCCCCC
                                                                                                                             TTACACAGCTTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG
GCAGAAGGAGAGGCGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTG
                                                     /*tag= c
/product= "Human mature GCREC-15"
                                                                                                                                                                                                                                                                                                                                                                                                       Human G-protein coupled receptor (GCREC-15) cDNA.
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/product= "Human GCREC-15"
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1. .1113
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21-AUG-2000; 2000US-0227054P.
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2000US-0232243P.
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/*tag= b
196. .1110
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13-SEP-2000; 2
15-SEP-2000; 2
22-SEP-2000; 2
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The invention relates to novel human G-protein coupled receptors (GCREC) and their encoding polynucleotides. GCREC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCREC is useful for diagnosing, treating and polyclonal antibodies. GCREC is useful for diagnosing, treating and polyclonal antibodies. GCREC is useful for hepatitis, psoriasis, cancer), a neurological disorder (e.g., palepssy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infaarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g., acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthmator, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infactions. GCREC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation,
                                                                                                                                                      New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarrays utilising fluids or tissues from patients to detect altered GCRBC expression. The present sequence is human GCRBC-15 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. GCREC is useful in Southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbant (ELISA)-like assays, and in
Graul
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  Kearney L,
Policky JL,
                                                                                                                                                                                                                                                                                            Claim 5; Page 148; 150pp; English.
g
j
Y, Tribouley
Lee EA, Ding
                                                                              2002-188744/24
                                                                                                       P-PSDB; AAE18654
  Ξ
                         BA,
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                         Warren
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Query Match 92.4%; Score 1064; DB 6; Length 1458;
Best Local Similarity 97.6%; Pred. No. 8.8e-22;
Matches 1121; Conservative 0; Mismatches 0; Indels 27; Gaps 3;

124 114 GCCGTCCTGCCGGGCCGAGGGCCGCCCTTCTCTCTTCACGGTCCTGGTGGTGACGCTG 184 304 364 354 CTAGTGCTGCTGGTCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG 234 64 09 5 ATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGTTGCCCTTGCCCTGGGACCCGAG ATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTTGGGAACCCCGAG ACCAGCAGCGGACCCCGAGCCCCGAGGGATACTCGGTTCGACCCCGAGCGGC 61 ACCAGCAG-----CGGGACCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGCGGC GAACTAGTGGCAGGCTGGCGGTGCCACCGAGCCTGGCGAGTGAGCTGTCGTCGTCGGGGCGA CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA CGTCGGCTGCTGGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCC------175 65 125 185 245 235 305 295 365 355 g d ò 셤 g ò g g 8 g ò ₹ 8

425 CIGIGCIGCCCCGCCGGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGAACGAGGGCC 484

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The invention relates to isolated human G-protein coupled receptor (GCREC) polypeptides and their biologically active fragments. GCREC and protein is useful in treating a disease or condition associated with an increase or decrease in expression of functional GCREC. The GCREC's are useful in the diagnosis, treatment and prevention of cell proliferative disorders (cancer, leukaemia, melanoma); neurological disorders (stroke, epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune inflammatory disorder (thyroiditis, haemolytic anaemia, AlDS, multiple sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris), gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis), metabolic disorders (diabetes); viral infections (herpes virus) and in the assessment of the effects of exogenous compounds on the expression of the nucleic acid and amino acid sequences. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human G-protein coupled receptor polypeptides and the use of these sequences in the diagnosis, treatment and prevention of diseases and in the assessment of exogenous compounds on the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu DAM, Tribouley CM;
Ramkumar J, Au-Young J;
V ML, Thornton M, He A;
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Lu DAM, Tr
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n JA, Yue H, Khan FA, Patterson C, Lu DAM
Walia M, Graul R, Ramkuu
t VS, Hernandez R, Walsh RT, Borowsky ML,
                                                                                                                                                                                                                    protein"
       '*tag= a
'product= "Human GCREC-8 protein"
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Pred. No. 6.1e-220;
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22-JUN-2000; 2000US-021354P.
29-JUN-2000; 2000US-0215209P.
07-JUL-2000; 2000US-0218358P.
14-JUL-2000; 2000US-0218935P.
19-JUL-2000; 2000US-0218935P.
21-JUL-2000; 2000US-0219354P.
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Best Local Similarity 97.7%;
Matches 1114; Conservative (
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Human cDNA encoding hydroxytryptamine receptor-like protein NOV8.

30-JUL-2002 (first entry)

standard; cDNA; 1155

ABK71923

ABK71923

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The invention relates to an isolated NOVX polypeptide selected from NOV1a, NOV1a, NOV1a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4b, NOV4b, NOV5c, NOV3b, NOV5b, NOV6b, NOV7, NOV7, Nov6b, uncreatia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disease, Huntington's disease, multiple sclerosis and manyotropic lateral sclerosis, acute brain injury (e.g. stroke, head injury and cerebral palsy), central nervous system disorders (e.g. depression, epilepsy and schizophrenia), lung disorders, reproductive disorders, disorders affecting carbohydrate metabolism (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness and pick's disease), disorders linked to abnormal angiogenesis, asthma, azospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, X-linked severe combined immunodeficiency, seizures, migraines, inflammation, autoimmune disorders, disorders affecting sleep, reproductive disorder; tissue disorder; thrombocytopaenia; migraine; angiogenesis; asthma; X-linked severe combined immunodeficiency; infinamation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disorder; hepatitis; fertility; hypertension; arteriosclerosis; ischaemia; rheumatoid arthritis; Grave's disease; wound healing. New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumors, lung disorders, hematopoietic disorders, autoimmune diseases and immune disorders. vascular disorder, infectious disease, anorexia, cancer, stroke, neurodegenerative disorder, Alzheimer's disease, acute brain injury, central nervous system disorder, depression; lung disorder; developmental disorder; endocrine disorder; , Taupier RJ, Vernet CAM, Colman SD; T, Malyankar UM, Shenoy S, Tchernev VT; an M, Burgess CE, Smithson G, Millet I; Gunther E, Ellerman K; Vernet CAM, C Claim 9; Page 59-60; 210pp; English. 15-SEP-2000; 2000US-0232675P.
15-SEP-2000; 2000US-0232676P.
18-SEP-2000; 2000US-0233802P.
18-SEP-2000; 2000US-0233802P.
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13-CCT-2000; 2000US-0240284P. 11-JAN-2001; 2001US-0260973P. 26-JAN-2001; 2001US-0264274P. 17-SEP-2001; 2001WO-US029115 09-MAR-2001; 2001US-0274862P Patturajan M, Tchernev VT, gene; NOVX; Syptek KA, Sorman L, Padigaru M, Pattull, TA, Stone D, (CURA-) CURAGEN CORP. WPI; 2002-383182/41. P-PSDB; ABG60235 VO200224733-A2 Homo sapiens. 28-MAR-2002. Mishra VS, BP.

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                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                     31;
                                                                                                                                                                             Length 1155;
                                                                                                                                                  Sequence 1155 BP; 175 A; 397 C; 356 G; 227 T; 0 U; 0 Other;
                                                                                                           mental retardation, psychotic and neurological disorders degeneration. The present sequence encodes a NOVX protein
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                                                                                                                                                                            Score 1016; DB 6;
Pred. No. 2.1e-210;
0; Mismatches 0;
                                                                                                                                                                            Query Match 88.2%;
Best Local Similarity 97.2%;
Matches 1087; Conservative
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878 CAGGTGAGCGGGACTCCTGGCGGGAGCAGAAGGAGGCGAGGCAGCCATGATGGTGGGG
                                                                   ATTCTGATTGCCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGC
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Pred. No. 4.5e-154;
0; Mismatches 13;
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P-PSDB; ADC86157.
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atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;

chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, depression, epilepsy, macular degeneration, lymphoma, melanoma,

unitiple sclerosis; oscionarthritis; oscionosis; Parkinson's diseas multiple sclerosis; oscionarthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; apain perception disorder; obesity; diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy.

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Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,

Pritchard

Fabre-Suver C,

Burmer G,

Miller M,

Brown JP,

WPI; 2002-066595/09

(LIFE-) LIFESPAN BIOSCIENCES INC

18-MAY-2000; 2000US-0205945P.

11-MAY-2001; 2001WO-US015332 11-MAY-2000; 2000US-0203217P

WO200185791-A1. Homo sapiens.

The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host

Disclosure; Page 119-120; 144pp; English.

stroke.

diseases listed in the specification. The probes and antibodies are also diseases listed in the specification. The probes and antibodies are also restful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GAHA polypeptide. The antibodies and nucleic acid probes as and nucleic acids and are used to detect the presence of the polypeptides and nucleic acids and are used to diagnose a variety of diseases or amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic acciding because depression, appliesy, macular degeneration, lymphoma, melanoma, multiple sclerosis, heumatoid osteoarthritis, osteoporosis, parkinson's disease, psoriasis, heumatoid osteoarthritis, osteoporosis, parkinson's disease, psoriasis, heumatoid 26; Length 977; Sequence 977 BP; 121 A; 356 C; 324 G; 176 T; 0 U; 0 Other; 20; Indels 64.7%; Score 745; DB 6; L 94.6%; Pred. No. 9.6e-152; iive 0; Mismatches 20; 803; Conservative Similarity Н Query Match Local Best Loca Matches ò

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Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma;

Human DNA for potential G protein-coupled receptor #11

(first entry)

12-MAR-2002

AAS98053;

ВР

AAS98053 standard; DNA; 977

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Oligonucleotides corresponding to conserved regions of known serotonin receptors were used in PCR of mouse brain RNA in presence of reverse transcriptuse and the products were sequenced. One product with homology to known receptors was labelled and used to probe a CDNA library in Lambda UniZAP. The 2036 bp sequence AAA70264 was identified and deduced to encode a protein having 7 hydrophobic domains which represents a novel serotonin receptor which was designated 5HT5b. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
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/note= "serotonin
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nes 911; Conservative
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                                                          ATCACACGGCACCTGCAGCACGCTGCGCACCCGGCAGCCGCGCGCTCGTTGCTCATGATC
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Pred. No. 4.9e-149;
0; Mismatches 202; Indels 27;
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21-DEC-2001; 2001US-0342472P.
28-MAR-2002; 2002US-00109532.
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Location/Qualifiers

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Serotonin; receptor; transmembrane; domain; kinase; phosphorylation; sensory; motor; behaviour; central nervous system; CNS; superfamily; G-protein; ligand-gated; ion channel; subfamily; human; rat; amplify; primer; PCR; amplification; brain; hypothalamus; indolamine; drug; hypothalamus; therapeutic; neurological; pathology; dementia; insomnia; Parkinson's disease, eating disorder; anxiety; migraine; headache; ss. BP. Rat MR22 serotonin receptor gene. AAQ72270 standard; cDNA; 2226 (first entry) 25-MAR-2003 24-MAY-1995 AAQ72270;

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GCGCCGTCCTGCCGGGCCGAGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGC 182

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361 AGAGCTGCAGTGAC----AGCCCAAGTTCCGGCAGAAGCATGGGATCCACCCCAGGGG

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The nucleotide sequence of the novel rat serotonin receptor MR22. The gene encodes a protein of 370 amino acids. The protein contains 7 cransembrane domains (TMDS), a putative N-linked glycosylation site and 4 putative sites for kinase C phosphorylation. Serotonin receptors a wide crange of sensory, motor and behavioural functions in the central nervous system (CNS). Serotonin receptors belong to at least two protein superfamilies: G-protein-associated receptors containing 7 TMDs (S-HT13/PbC/d/d/s-5-HT2) and ligand-gated ion channel receptors superfamilies: G-protein-associated receptors presented in the patent represent prototypes that fall into three new serotonin subfamily classifications: 5-HT16-like (rat MR77 - AAQ72271 and human MR77 - AAQ72272), 5-HT5 (subdivided into 5-HT5lpha, rat REC17 - AAQ72269 and 5-HT5 (brit the receptors were cloned by amplification based on conserved amino contain sequences and used in two rounds of nested PCR amplification on a crat brain hypothalamic cDNA template. In the second round of amplification degenerate primers corresponding to conserved residues found in the TMDs manual fragments were cloned into pBluescript vectors. The plasmid fragments were used to samplify only those receptors. The resultant fragments were used to samplify only those receptors. The resultant fragments were cloned into pBluescript vectors. The plasmid fragments were used to screen a rat hypothalamus contains may be used in methods for determining luman in receptors, dray screening and altering expression of serotonin receptors. Grand therspeutic treatments involving human in receptors and therefore the receptors are contained the receptors.
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The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                              diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                               Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2961
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Pred. No. 2.2e-148;
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                                                                                                                           toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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          ADB52419 standard;
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Query Match Best Local Similarity

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The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host call comprising an expression vector comprising the GPCR sequence. The polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulators of the polypeptides. Which function as modulators, activators, identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GAL4 polypeptide. The antibodies and nucleic acid probes as described above can be used to diagnose a variety of disease or disorders in which GPCRs are involved e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, choosis, chronic costume degeneration, lymphoma, melanoma, multiple sclerosis,
ACACAGCTITITAACAAGAACTACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGAT 1142
                                                     1354 ACKCGGCCTTTAATAAGAACTACAACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGAT 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma; psoriasis; osteoarthritis; osteoporosis; parkinson's disease; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; cardiovascular activity disorder; pain perception disorder; dene therapy.
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RESULT 14

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arthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and mency disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds be used to increase the expression of galanin receptor (GAL4) can be used to treat obesity, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide
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                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                            Score 721.2; DB 6; Length 1090;
Pred. No. 1.4e-146;
0; Mismatches 13; Indels 26;
                                                                                                                                                                                                  Sequence 1090 BP; 157 A; 364 C; 372 G; 197 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCT 823
                                                                                                                                                                                                                                   62.6%;
                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2.
Best Local 775; Conservative
                                                                                                                                                                     of the invention
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The invention relates to single nucleotide polymorphisms in the gene encoding human 5-hydroxytryptamine (serotomin) receptor 5A (HTRSA). A method for haplotyping the HTRSA gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and
                                                                                              Human; 5-hydroxytryptamine receptor 5A, HTR5A; serotonin; gene; ds; neuroprotective; neurological disease; depression; epilepsy; gene therapy; single nucleotide polymorphism; haplotype pair; chromosome 7q36.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Serotonin) Receptor reliability in drug
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                                                                            (HTR5A)
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                                                                            5A
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                                                                            Juman 5-hydroxytryptamine receptor
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the HTRSA haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair. This method is useful in genotyping, pair of the HTRSA gene can be identified by comparing the frequency of the HTRSA gene can be identified by comparing the frequency of the haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype frequency in the trait population, where a higher haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. HTRSA and its corresponding DNA are used for studying the expression and function of HTRSA, and in screening for candidate drugs to treat diseases related to HTRSA activity, such as neurological disorders, including depression and epilepsy. This sequence represents the DNA encoding the human HTRSA polypeptide
   gene is defined by one of
   the copies of the
   whether one of
555555555555555555X&
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Sequence 1074 BP; 182 A; 366 C; 284 G; 242 T; 0 U; 0 Other;

113 ACCCCGAGCGCCGCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTG 172 126 232 186 292 246 352 306 412 363 414 532 474 592 534 652 594 712 654 714 832 765 GCCGGAGCCTGTCTGTGCCCCCCCCCGCCGGCCTCGGGAACGTGGCGGCCATCGCCCTGGGC 472 GAAGTGGTGTTCACGCCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGACTCC 892 <u> AGCCTCGGCAAAGACGACCTGCGCCCCAGCTCGCCCCTGCTCTCGGTCTTCGGAGTGCTT</u> eccercicedanerecreenesecececreenearececreaeceresecreenesecare TTGCTCATGATCGCGCTCGCCCGGGTCGCCGTCGCCGTCATCGCCCTCGCGCCGCTGCTC rcchaceccererrereacenasecerreracecerececererererererer GIGGIGACGCIGCIAGIGCIGCIGAICGCIGCCACIIICCIGIGGAACCIGCIGGIICCG GTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACG GTGTACTGGAAGATCTACAAGGCTGCCAAGTTCCGCGTGGGCTCCAGGAAGACCAATAGC 127 ATTCTCACCTTGCTGGGCTTTCTGGTGGCGGCGACGTTCGCCTGGAACCTGCTGGTGCTG GCGACCATCCTCCGTGTACGCACCTTCCACCGGCGTGCCCCACAACCTGGTGGCATCCATG GCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTG TCGACCGGGCGACGTCGGCTGCTGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGAC -----TGCTTTGCTGCACGGCCAGCATCTGGAACGTGACGCCCATAGCCCTGGAC TTTGGCCGGGGGGGGGGGGGGCGCTCCAGCGCTGCCAGGTGAGCCGGGAACCC TCCTATGCCGCCTTCTCCACCCGCGCGCCTTCCACTGCCGCTTGGCGTGGTGCCGTTT CTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCT TTTGGCTGGGGAGAGGTGCTCTGAGGGCAGCGAGGAGTGCCAGGTAAGCCGCGAGCCT Gaps 24; Score 497.6; DB 6; Length 1074; Pred. No. 3.6e-98; 0; Mismatches 279; Indels 24; Query Match Best Local Similarity 70.6%; Matches 729; Conservative Ę Ö 29 173 187 293 353 307 413 364 473 415 533 475 535 653 595 713 655 773 임 ŏ Db δ à q à g à g ò ద à g ò Ob δ d à g δ g à g à qq

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RESULT ABZ428 ID A	15 28 BZ42828 st	andard; DNA; 1074 BP.
ž S	ABZ42828;	
X E	04-MAR-2003	(first entry)
₹ 83	Human 5-HT5A	receptor nucleotide SEQ ID NO:445.
ž ž	G protein-con	upled receptor; GPCR; antigenic peptide; gene therapy;
K K K K	G protein-cor G protein-cor growth-relate immunological	pried receptor modulator; antibody; immune-related disease; and disease; cell regeneration-related disease; l-related cell proliferative disease; autoimmune disease;
& & & & 3	Alzheimer's costeoporosis; graft versus	isease; atherosclerosis; infection; osteoarthritis; allergy; cardiomyopathy; inflammation; Crohn's disease; diabetes; host disease; multiple sclerosis; pain; district accounts to the control of the con
Z Z Z Z	mental retard hypertension; ulcer; gene;	potential retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; ds.
X 8	Homo sapiens.	
X M	WO200261087-A	12.
X & :	08-AUG-2002.	
PF	19-DEC-2001;	2001WO-US050107.
4 E \$	19-DEC-2000;	2000US-0257144P.
4 & \$	(LIFE-) LIFESPAN	SPAN BIOSCIENCES INC.
4 E \$	Burmer GC, F	Roush CL, Brown JP;
888	WPI; 2003-046 P-PSDB; ABP81	003-046718/04. ; ABP81980.
XX TAGA	New isolated (GPCR), usefuin which GPCR autoimmune di	New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
PS	Disclosure; F	Fig 1; 523pp; English.
488888	The present any one of 16 acids. Also cprotein-coupland (2) an is	The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABB83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or

CAGATGGTGTTCACGGTCC---GCCACGCCACCGTCACCTTCCAGCCAGACAGGGACACG 822

avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, call regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alabiemer's disease, atherosclerosis, bacterial, fungal, protogoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention Sequence 1074 BP; 182 A; 366 C; 284 G; 242 T; 0 U; 0 Other;

43.2%; Score 497.6; DB 7; Length 1074; larity 70.6%; Pred. No. 3.6e-98; Conservative 0; Mismatches 279; Indels 24; Local Similarity es 729; Conserv Query Match Best Loca Matches

232 113 ACCCCGAGCGGCGCCGTCCTGCCGGGCCGAGGCCGCCCTTCTCTGTCTTCAGGTCCTG 172 126 127 ATTCTCACCTTGCTGGGCCTTTCTGGTGGCGGCGACGTTCGCCTGGAACCTGCTGGTGCTG 186 292 GTGGTGACGCTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCG GTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACG 173 à g à

GCCGTCTCGGATGTCCTGGTGGCCGCGCTGGTCATGCCGCTGAGCCTGGTGCATGAGCTG 306 GCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTG TCGACCGGGCGACGTCGCTGCTGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGAC 247 293 353

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1012 ATCCCCGCCATCTGGAAAAGCATCTTCCTGTGGCTTGGCTACTCCAACTCCTTCTTTAAC 1002 CCCCTGATCTATACGGCTTTCAACAAGAACTACAACAGCGCCTTCAAGAACTTCTTTTCT 1062 TGGCGGGAGCAGAAGAAGAAGAAGGAGCCGCCTCATGGTGGGCATCCTCATTGGCGTGTTC 882 GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCC 892 --CICACCCATATCCGAAGCTGTGGAGGTGAAGGACTCTGCCAAACAGCCC 765 TGGCGGGAGCAGAAGGAGAGAGCGAGCCATGATGGTGGGGAATTCTGATTGGCGTGTTT GIGCIGIGCIGGAICCCCTICTICCIGACGGAACTCAICAGCCCACTCTGIGCCTGCAGC CCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACT cagaridericacidence---eccacecaceiroacentecadecagaadada AAGCAGAGATGA 1144 1063 AGGCAACACTGA 1074 Ė 943 1013 1003 1133 715 833 823 883 893 953 1073 Dp q g ð qq à 장염 ∂ à ò

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OM nucleic - nucleic search, using sw model
                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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		geno	mic sur	rvey se	sednenc	ce.		
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KEYWORDS		GSS.						
SOURCE		Ното	sapier	(human) st	an)			
ORGAL	Σ	Homo	sapier	SI				
		Euka	ryota;	; Metazoa; (Entheria:	μ. 	Chordata; Craniata; Drimates: Catarrhit	a; Vertebrata; Euteleostomi; ini: Hominidae: Homo	
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AUTHORS		Clar	k, A.G.,	Glano	vski	, Glanowski, S., Nielson, R.,	Thomas, P., Kejari	
		Todd	, М.А.	Tanenb	aum,	vello, D.	L., Lu, F., Murphy,	
		Ferr	iera, S.	., Wang	0 7	с.н., whi	e,T.J., Sninsky,J.J	
TITLE		Infe	rring r	and car	ral.	ŭ	from human-chimp-mouse orthologous	
AGTIOT.		gene	trios) (5652)	2)	(2002) (2003)		
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 640) Volik, S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.
End-sequence profiling: Sequence-based analysis of aberrant genomes 27709111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MCF7_1) " / MCF7_1) " / MCF7_1) Micros "Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
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                                                                                                                                                                                                                                                                                                                     Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
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Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_Xref="taxon:9606"
/clone="MCF7_1-1113"
/sex="female"
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                                                                                                                                                                                                                                                                                                                                                              http://www.genomex.com
Class: BAC ends.
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Best Local Similarity 92.2%;
Matches 535; Conservative
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KEYWORDS
SOURCE
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Gaps

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GATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCGGAGAGCTGTGCTGCCGTTGCC

724

Homo sapiens (human)

GSS.

ACCESSION

Homo sapiens

667

609

607

699 787 907

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ымвиьв59
AGENCOURT_6513650 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5731557
5′, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1099)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can febund through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
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Sciurognathi; Muridae; Murinae; Mus
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Direct Submitsion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Mus musculus HTR5A gene, VIRTUAL TRANSCRIPT, partial sequence,
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1. 1074
/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV destroyed); Site 2: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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BI489745 906 bp mRNA linear EST 28-AUG-2001 603032245F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173354 5',

mRNA sequence. BI489745

DEFINITION

LOCUS

RESULT 6 BI489745

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/lab host="DH108"
/clone lib="NUH MGC l15"
/clone lib="NUH MGC l15"
/clone lib="NUH MGC l15"
/clone lib="NUH MGC l15"
/note="Organ: pooled brain, lung, testis; Vector:
pcWV-SPORTE; Site l: Not1; Site 2: EccRV (destroyed); RNA source anonymous pool of 6 male brains, age for Library is male lung, age 27; and l male testis, age 69. Library is oligo-dT primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 906)
III-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1431 row: j column: 11
High quality sequence stop: 826.
High quality sequence stop: 826.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
Homo sapiens (human)
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                                                             Homo sapiens
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1027 bp DNA linear GSS 01-SEP-2000 nigroviridis genome survey sequence T3 end of clone library A from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                               CCGCCTTCTCCACCCGCGCGCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACC 719
                                                                                          Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Enteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 20296633
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AL344524.1 GI:8238294
GSS; genome survey sequence.
Tetraddon nigroviridis
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IMAGE:5173354, mRNA sequence.
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//db xref="taxon:9606"
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/db xref="taxon:9606"
/db nost="mAcp99801111431; IMAGE:5173354"
/lab host="mB108"
/clone_lib="NIH_MGC_115"
//clone_lib="NIH_MGC_115"
//clone='lorgan: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (EcoRV site is oligo-dr.) in the state of the site of the state of the site of the state of the site of the state 
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                                  Homo sapiens

Busaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Busaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 539)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,

Radelof, U., Schneider, D. and Korn, B.

Human Unigenset - RZPD3

Unpublished (2003)
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RZPDLIB; I.M.A.G.E. CDNA. Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cg1-
bin/showLib.l.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Resourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: 49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (cloneGarzpd.de) for further information. Seq prin
M13u, Primer sequence: CGTTGTAAAACGACGCCAGT.
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP9998J111431.
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Direct Submission

Birect Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="0.38018"
/clone llb="A"
/clone llb="A"
/note="Genoscope sequence ID : COAA038BH09Al-end : T3"
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0; Mismatches 171; Indels
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RESULT 9 BI603546/c

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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninoi (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llnl.gov
Plate: LLAM1725 row: o column: 11
High quality sequence start: 2
High quality sequence start: 2
High quality sequence story: 720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BI603546 893 bp mRNA linear EST 07-SEP-20
603244448Fl NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5287138 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vec
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/db_xref="taxon:9606"
/clone="IMAGE:5287138"
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BI603546.1 GI:15496485
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                        TGCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGG
                                                                                                    457 IGCTGGTGCTGGCGACCATCCTCCGTGTACGCACCTTCCACCGGGTGCCCCACAACCTGG
                                                                                                                                                                                                                                                      CGAGTGAGCTGTCGACCGGGGGGACGTCGGCTGGGCCCGGGAGCCTGTGCCACGTGTGGA
                                                                                                                                                       TGGCCTCGACGCCCGTCTCGGACGAACTAGTGGCAGCGTGGCGATGCCACCGAGCCTGG
                                                                                                                                                                                                                                                                                                                                                     TCTCCTTCGACGCCGGAGCCTGTCTGTGCTGCCCCGCCGGCCTCGGGAACGTGGCGGCCA
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
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Fax: 402 762 4390
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Bos taurus
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235 TAGCCCTGGACCGCTACTGGTCCATCACGCGCCACATGGAATACACGCTCCGCACCGCA 176
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Tissue Procurement: MixLos Palkovits, M.D., Ph.D.

ToShiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 9436

Web site: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAR Plate: 63 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                           175 AGTGCGTCTCCAACGTCATGATCGCGCTCACCTGGGGCACTCTCCCGCTGTCATCTCTCTGG
                                                                                                                                                                                                                            ccccccicirriridecredecadadaceracirereagecadeageagrecadeara
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                                                                             GCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCG
                                                                                                                                                                              582 GGCGGCTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGA
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Location/Qualifiers
1. .2683
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/mol type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE:5287138"

/tissue type="Brain, hypothalamus"

/clone lib="with MGC_96"

/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2683 bp mRNA
Homo sapiens, clone IMAGE:5287138, mRNA.
BC031272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC031272.1 GI:22658348
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                    /tissue_type="pooled"
/lab host="DH10B"
/clone_lib="MARC 2000"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                   GCACACGCTGCGCACCCGCAGCCGCGCTTGCTTGCTCATGATCGCGCTTCGCCCCGGGTGCC
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                                                                                                                                                                                                24; Gaps
                                                                                                                                                                   Score 247.6; DB 12; Length 583;
Pred. No. 4.3e-35;
0; Mismatches 170; Indels 24;
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                organism="Bos taurus"
                           /mol_type="mRNA"
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Dupublished (1999)
Conteat: Robert Strausberg, Ph.D.
Email: cgapbe refmail.nih.gov.
Tissue Procurement: Mixlos Palkovits, M.D., Ph.D.
Tissue Procurement: Mixlos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10689 row: j column: 15
High quality sequence stop: 470.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ceeccanaeccerneaccecnacreercearcacececacareaaracacecreeca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAACCTGCTGGTGCTGGACCATCCTCGTGTACGCACCTTCCACCGCGTGCCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 ACTIGGIGGCCICGACGGCCGICTCGGACGAACTAGIGGCAGCGCTGGCGAIGCCACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 Accresigacarcareacercicasararcasaraceasaces
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%; Score 239.6; DB 12; Length 472; llarity 71.9%; Pred. No. 1.2e-33; Conservative 0; Mismatches 124; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="hypothalamus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_96"
/note="Organ: brain; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4799726"
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861

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969

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BB628489 RIKEN full-length enriched, 16 days neonate cerebellum Mus musculus CDNA clone 9630009M09 5', mRNA sequence.
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                                                                                                                                                               634 TCGGATGTCCTGGTGGTCTCTGGTGATGCCTCTGAGCCTGGTGAGCGAGTTGTCCGT- 692
                                                                                                                                                                                                                                                                359 GGGCGACGTCGCTGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGA 418
                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(58C), Yokhama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,

CarLittp://genome.gsc.riken.go.jp,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     862 TCATGATCGCGATCACCTGGGCACTGTCCGCGCCTCATTGCTCTCGCCCGCTGCTTTAGG 921
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                  574 ATCCTGCGTGTCCGCGCCTTCCACCGCGTGCCACATAACTTGGTGGCCTCGACAGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                        419 GCCTGTCTGTGCTGCCCCGCCGCCGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     753 TGCTG------CACCGCAGCATTTGGAACGTGGCTGGCATCGCCCTGGATCGCTAC
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                                                                                                            TCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACC
Mus musculus (house mouse)
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Fax: 81-45-503-9216
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph
                                                                                                 BI411238 929 bp mRNA linear EST 14-AUG-2001
602964578F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5120035 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pt7773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 ACCAGCAGCGGACCCGGGACCCCAAGCCCGAGGGATACTCGGTTCGACCCCGGAGGGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTCCTGCCGGGCCG--AGGGCCGCCTTCTCTGTCTTCA-CGGTCCTGGTGGTGACG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 CTCATCTTGCCTGGTCCGCGAGCCTGAACTTCTCTGCTTTCACCTGTGCTTGTGGTGACT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIGCTAGIGC -- TGCTGATCG - CIGCCACTITCCIGIGGAACCIGCTGGTTCCGGTCACC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 CTACTTGGTGTTTGCTGATCGTTTGCCACTTTCTTATGGAATCTGCTAGTTCTGGTGACT 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 ATCCCGCGGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGCGTTGCCCTTGCCCTGGGACCCGAG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 -TGAGAGCTGCAGTGACAGGCCCAAGTTCCGTGCAGGAGCATGGGATCCACCCCAGGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov | Plate: LLAM11292 row: | column: 20 High quality sequence start: 177 High quality sequence stop: 928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                        BI411238.1 GI:15172161
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                                                                                                                                                                          mRNA sequence.
BI411238
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Best Local Similarity
Matches 421; Conserv
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                                                                                                                                       DEFINITION
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VERSION
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TITLE
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                               RESULT 13
BI411238
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Query Match
Best Local S
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                                                                                                         RESULT 15
BM861710/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1043 TGGCTTGGCTACTCCAATTCTTTCTAACCCCCCTGATTTACACAGCTTTTAACAAGAAC 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5, 6] GAGAGAGAGAACGATCCAAGAGCTCTTTTTTTTTTTTVN 3'), cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTTCACGGCACATTGCAAAGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TG-----AAGAATGCTACACAACATCCCCAGATGGTGTTCACGGTCC---GCCATGCC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 CTCATGGTGGGCATCCTCATCGGAGTGTTTGTGCTCTGCTGGTTCCCTTTCTTCGTCACA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTACCTGCCGCTGTGCGTGCTCTTTGTGTACTGGAAAATTTACAGGGCGGCGAAA 61
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 GAGCTCATCAGTCCCCTGTGTTCCTGGGACGTCCCTGCCATCTGGAAGAGCATCTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 TITICGITITCGCCCGCCCGCCGGAGAGCTGTGCTGCCGTTGCCGGCCACCAIGCAGGTGAGG
                                                                                                                                           Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%; Score 198.4; DB 10; Length 660; 69.0%; Pred. No. 4.3e-26; tive 0; Mismatches 131; Indels 12;
                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cerebellum"
/dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                               'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           /clone="9630009M09
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                                                                                                                                                                                                                                                           .660
                                                                                                                                                                                                                   mouse tissues.
                                                                                                 Alzawa, h., fuk
Hayashizaki, Y.
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Best Local Similarity
Matches 319; Conserv
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/done libe "Sugano SuD adult male".
//done "Vector: pMB18S-F13; Site 1: Drall1 (CACCATGTG); Site 2: Drall1 (CACTGTGG); Libe 1: Drall1 (CACTGTGG); Mile an oligo(dT) primer [ATGGCCTTTTTTTTTTTTTTT];
//double-stranded cDMA was ligated to a Drall1 adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Drall1 sites of the pME18s-F13 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert: Size selection was performed to exclude fragments cl. Skb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTGCTGTAAAACTGC and 3' end primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L (Jark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watterston, R. and Wilson, R., Watterston, R. and Wilson, R. Unpublished (1998)

L Unpublished (1998)

L Onter ESTS: Eydseo, J., Contact: Stephen L. Johnson Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314, 286, 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: zbrafish@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: T7 from Gibco
                                                                                                                                                                                                                                                          BM861710 655 bp mRNA linear EST 07-MAR-2002 fy49e02.xl Sugano SJD adult male Danio rerio cDNA clone IMAGE:5603043 3' similar to SW:5H5A_HUMAN P47898 5-HYROXYTRYPTAMINE SA RECEPTOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 CCGCATAACTTGGTGGCCTCGACGCCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 655)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 173.8; DB 12; Length llarity 64.5%; Pred. No. 1.4e-21; Conservative 0; Mismatches 157; Indels
1103 TACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGATGA 1144
                                        410 TACAGCAGTGCTTTCAAGGTCTTCTTCTCCAAGGCAACAATGA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev stage="adult"
/lab_host="DH10B (phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="whole body"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 525.
Location/Qualifiers
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/db_xref="taxon:7955"
/clone="IMAGE:5603043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM861710.1 GI:19229392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
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5 CCCCACAACCTTGTAGCCTCCCATGGCCATATCTGACGTCATGGTGGCAGCTTTGGTGATG 596	CCACCGAGCCTGGCGAGTGAGCTGTCGACGCGGCGGGCGG	5 CCTCTCAGTCTGGTCCACGAGCTGAACGGCCGTCGGTGGGAAGCTGGGTCGCGTTCTC 539	9 TGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGTCTGT		PARCGIGGGGCCATCGCCCTGGGCCGCGACGGGCCATCACACGGCACCTGCAGCACACG 508	7 AACGIGACCGCAAIAGCCCTCGACCGITACTGGTCCAIAACTCGACACCTGGAGTACACC 428	TGCGCACCCGCAGCCGCGCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTGC 568	Thaagacccggaagaagatctccaatgtgatgatcgggttaacctggctgctttcatct 368	9 CTCATCGCCCTCGCCCGCTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAG 628	7 GITATITCGCTCTCGCCTCTGTITGGCTGGGGTGAGACGIAITCGGAGGAGAACAIG 311	9 CGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACCGCGGCGCCTTCCAC 688	O GAGTGCCAGGTGAGCCGTCTTACACCATCTTTTCCACATTCGGGGCCTTCTAT 251	CTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGT 748	CTGCCTCTCTGTGTTGTGTCTTTGTCTACAAAGATTTACAAAGCTGCTACTTCCGT 191	9 TTCGG 753	0 ATTGG 186	
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Search completed: September 7, 2004, 17:13:12 Job time: 2870 secs

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7, 2004, 16:25:27; Search time 586 Seconds (without alignments) 9771.633 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 15, Appl	Sequence 9, Appli	Sequence 11, Appl	Sequence 34, Appl	Sequence 25, Appl	Sequence 29, Appl			Sequence 1, Appli	Sequence 445, App	Sequence 39, Appl	37,	Sequence 15, Appl	-
) THE P. CO.	ព	US-09-976-782-15	US-09-823-187-9	US-09-823-187-11	US-10-333-946-34	US-10-311-671-25	US-09-954-342-29	US-10-017-161-697	US-10-292-798-609	US-10-109-532A-1	US-10-225-567A-445	US-10-345-680-39	US-10-345-680-37	US-10-352-684A-15	US-09-823-245A-617
		101	10	10	17	12	10	15	16	15	15	15	15	16	13
	* Query Match Length DB	1152	1150	1150	1458	1119	1155	3086	3086	2061	1074	1074	1159	1159	2700
	% Query Match	100.0	92.7	92.4	92.4	92.0	88.2	65.6	65.6	63.6	43.2	43.2	43.2	43.2	43.1
	Score	1152	1068	1064.8	1064	1060	1016	756.2	756.2	732.8	497.6	497.6	497.6	497.6	496
	Result No.	1	7	e	4	S	9	7	8	6	10	11	12	13	14

; ORGANISM: Homo sapiens US-09-976-782-15

ru 44.	Sequence 21329, Sequence 213298, Sequence 213298, Sequence 213299,	Sequence 213299, Sequence 4, Appli Sequence 43, Appl Sequence 754, App	Sequence 42, Appl Sequence 40, Appl Sequence 42, Appl Sequence 19, Appl Sequence 52, Appl	Sequence 40, Appl Sequence 1077, Ap Sequence 1, Appli Sequence 1197, Ap	Sequence 32, Appl Sequence 448, App Sequence 12, Appl Sequence 15, Appl Sequence 1, Appli Sequence 1, Appli
US-09-826-509-446 US-09-750-373-5 US-10-029-386-9467 US-09-750-373-4 S US-10-029-386-2940	US-10-029-386-16640 US-10-027-632-21329 US-10-027-632-21329 US-10-027-632-21329		US-10-001-073-42 US-10-001-073-40 US-10-345-680-42 US-10-225-567A-19 US-10-101-510-52	US-10-345-680-4 US-10-305-720-1 US-10-352-684A- US-10-305-720-1 US-09-954-531-99	US-10-717-557-32 . US-09-28-6-509-448 US-09-993-844-12 US-10-241-313-15 US-10-060-795B-1 US-10-060-795B-10
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ALIGNMENTS

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RESULT I
RESULT I
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PUBLICATION NO. US203190715A1
Sequence 15, Application US/09976782
Sequence 15, Application NG 09976782
Sequence 15, Application NG 09976784
SERVERAL INFORMATION:
APPLICATION NO. US2003190715A1e1 Proteins and Nucleic Acids Encoding Same TITLE OF INVERTION: NO. US2003190715A1e1 Proteins and Nucleic Acids Encoding Same FILE REPERENCE: 2140.2157
CURRENT FILING DATE: 2001-10-12
PRIOR PLING DATE: 2001-10-12
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2001-10-18
PRIOR PLING DATE:
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Qy 1021 CATCTGGAAAAGCATATTCTGTGGCTTGCTCCAATTCTTCTTCACCCCCTGAT 1080 Db 1021 CATCTGGAAAAGCATATTCTGTGGCTTGGCTCCCAATTCTTCTTCAACCCCCTGAT 1080 Qy 1081 TTACACGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG 1140 Db 1081 TTACACAGGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG 1140 Qy 1141 ATGAACACAGGG 1152 Db 1141 ATGAACACAGGG 1152 Db 1141 ATGAACACAGGG 1152	Sequence Application US/0922187	
Query Match 100.0%; Score 1152; DB 10; Length 1152; Best Local Similarity 100.0%; Pred. No. 7.2e-314; Indels 0; Gaps 0; Matches 1152; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy CCCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	121 CGGCGCCCCCCCCCCGGGGCCCCCCCCCCCCCCCCC	

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                                                                                                                                                               GENERAL INVEXEMENTION:

APPLICANT: Burgees, Catherine
APPLICANT: Burgees, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Dadiuder, Kumud
APPLICANT: Padiuder, Kumud
APPLICANT: Padiuder, Rorard A
APPLICANT: Spaderna, Steven K
APPLICANTON NUMBER: 60/195, 343
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-14
PRIOR
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Best Local Similarity 97.5%; Pred. No. 2.3e-289;
Matches 1123; Conservative 0; Mismatches 2;
                                                                               ; Sequence 11, Application US/09823187; Publication No. US20030096952A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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US-09-823-187-11
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; OTHER INFORMATION: Incyte ID No. US20040023252A1 7476053CB1
US-10-333-946-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R. APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K. APPLICANT: HAFALIA, APPLI J.A.; YAO, Monique G. APPLICANT: HAFALIA, APPLI J.A.; YAO, Monique G. APPLICANT: LU, Yan; TRIBOULEY, Catherine M. APPLICANT: LU, Yan; TRIBOULEY, Catherine M. APPLICANT: GRAUL, Richard C.; WARREN, Bridget A. TILE, ELTERINE A.; DING, Li TILE, DY INVENTION: G-PROTEIN COUPLED RECEPTORS FILE REFERENCE: PI-0176 USN
CURRENT APPLICATION NUMBER: US/10/33,946
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/221,478
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-15
PRIOR 
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Pred. No. 4.2e-289;
0; Mismatches 0;
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Best Local Similarity 97.6%;
Matches 1121; Conservative
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Sequence 34, Application US/10333946
Publication No. US20040023252A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael
APPLICANT: RAVIZU, Chandra S.; LAL, Preeti G.
APPLICANT: BURFORD, Noil; YUE, Henry
APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.

RESULT 4 US-10-333-946-34

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                                                                                         APPLICANT: HERNANDEZ, Roberto
APPLICANT: HERNANDEZ, Roberto
APPLICANT: HERNANDEZ, Roberto
APPLICANT: HERNANDEZ, Roberto
APPLICANT: HORNANDM, Michael B.
APPLICANT: THORNIOM, Michael B.
APPLICANT: THORNIOM, Michael B.
APPLICANT: HE, Ann
TITLE OF INVENTION OF SEPOTEIN COUPLED RECEPTORS
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
TITLE OF INVENTION OF SEPOTEIN COUPLED RECEPTORS
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/213,954
PRIOR APPLICATION NUMBER: 60/213,954
PRIOR PILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/215,209
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,936
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,936
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/219,154
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/219,154
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/219,154
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OTHER INFORMATION: Incyte ID No: 7474977CB1
RAMKUMAR, Jayalaxmi
AU-YOUNG, Janice K.
ELLIOTT, Vicki S.
HERNANDEZ, Roberto
WALSH, Roderick T.
BOROWSKY, Mark I.
THORNTON, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1114; Conserv
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Publication No. US20040072996A1
GENERAL INFORMATION:
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TRIBOULEY, Catherine M.
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APPLICANT: LAL, Preeti G.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HAFALIA, April J. A.
APPLICANT: GANDHI, Ameran R.
APPLICANT: GANDHI, Ameran R.
APPLICANT: GANDHI, Ameran R.
APPLICANT: GANDHI, Ameran R.
APPLICANT: GRIFFIN, Jennifer A.
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KHAN, Farrah A.
ARVIZU, Chandra S.
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CHAWLA, Narinder K.
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YAO, Monique G.
YANG, Junming
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                                                                                                                                                                                                                                       Length 3086;
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                                                                                                                                                                                                                                     Score 756.2; DB 15;
Pred. No. 2.4e-202;
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Best Local Similarity 95.4%;
Matches 810; Conservative
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                                                                   470 GCGGCCATCGCCCTGGGCCGCGACGGGCCATCACACGCCACCTGCAGCACCACCACCACGCGCGC
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                                                                                                                                                                                                                                                                   CTTGGCGTGGTGCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTCGGC
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                                                GCGGCCATCGCCCTGGGCCGCGACGGGCCATCACACGGCACCTGCACGCTGCGC
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Publication NO. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, MAKIKO

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ARGURAL NOVEL G PROTEIN-COUPLED RECEPTORS

TILLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PATCHIN VET: 2.1

SEQ ID NO 697

LENGTH: 3086
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GIGIGGALCICCTICGACGCC
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GENERAL TRACES.

APPLICANT: Allen, Keith D.

TITLE OF INVENTION: TRANSGENIC MICE CONTAINING 5-HTSB.

TITLE OF INVENTION: SEROTONIN RECEPTOR GENE DISRUPTIONS.

FILE REPERBNCE: R-601

CURRENT APPLICATION NUMBER: US 60/280,533

PRIOR PELING DATE: 2002-03-29

PRIOR PLING DATE: 2001-03-29

PRIOR FILING DATE: 2001-12-21

FRIOR FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 1
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Best Local Similarity 79.9
Matches 911; Conservative
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publication No. US2003235833A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AAFIAMA, YUTAKA
APPLICANT: AAFIAMA, YUTAKA
APPLICANT: ABURATANI HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFREENCE: 084335/166
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR PILING DATE: 2001-12-18
PRIOR PALLING DATE: 2001-12-18
PRIOR PLILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
SOFTWARE: PACH OF THE COUPLED FROM THE CO
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larity 95.4%; Pred. No. 2.4e-202;
Conservative 0; Mismatches 13; IndelB 26;
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LOCATION: (2218)..(2886)
                                                                                                    2638 AACGTTGCT 2646
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FEATURE:
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FEATURE:
LOCATION: source
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US-10-292-798-609
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oy Oy	426 CTCATCTTGCCCGGCCGCGCCCTTCTCTGCTTTCACCGTGCTTGTGGTGACTCTA 485 185 CTAGTGCTGCTGCTGCCACTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG 244	; APPLIC ; APPLIC ; TITLE ; FILE F	APPLICANT: Brown, Joseph P. APPLICANT: Burmer, Gleina C. APPLICANT: Roush, Christine L. TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
oy Op	245 CGGGTCCGTGCCTTCCACGGGGGGCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC 304	CURR CURR PRIO PRIO	CURRENT APPLICATION NUMBER: US/10/225,567A CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: 60/257,144 PRIOR FILING DATE: 2000-12-19
δλ Op	305 GAACTAGTGGCCAGCCTGGCGATGCCTGGCGAGTGAGCTGTCGACCGGGCGA 364	NUMB SOFT SOFT SEQ I	NUMBER OF SEQ ID NOS: 2292 SOFTWARE: Patentin version 3.1 EQ ID NO 445 LENGTH: 1074
AQ qa	365 CGTCGGCTGCTGGGCCGGAGCCTGTGCGAGTCTCCTTCGACGCCGGAGCCTGT 424	; TYP ; ORG US-10-2	; TYPE: DNA ; ORGANISM: Homo sapiens US-10-225-567A-445
oy an		Query Best Match	Query Match 43.2%; Score 497.6; DB 15; Length 1074; Best Local Similarity 70.6%; Pred. No. 1.1e-129; Matches 729; Conservative 0; Mismatches 279; Indels 24; Gaps 4;
čo a	485 ATCACACGGCACCTGCAGCACCCGCACCCGCGCGCGCGTGGTTGCTCATGATC 544	√o qa —-	113 ACCCGAGGGGCGCGTCTGCCGGGCGGCCGCCTTCTCTGTCTTCAGGGTCCTG 172
λό q	545 GCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCCGCTGCTCTTTGGCCGGGGC 604	λο qa	173 GTGGTGACGCTGCTGCTGCTGCTGCCACTTTCCTGTGGAACCTGCTGGTTCG 232 127 ATTCTCACCTTGCTGGGCGTTTCTGGTGGCGGCGACGTTCGCCTGGAACCTGCTGGTGCTG 186
oy Pb		co o	233 GTCACCATCCCGGGGTCCGTGCCTTCCACCGCGTGCCGTAACTTGGTGGCCTCGACG 292
상 엽		Qy	293 GCCGTCTCGGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTCAGCTG 352
දු දු		QV QD	353 TCGACCGGGCGACGTCGCTGGCGGAGCCTGTGCCACGTGTGGATCTCCTTCGAC 412
S d		Qy	413 GCCGGAGCCTGTCTGTGCTGCCCCGGCCCTGGGACGTGGCGCCCATCGCCTGGGC 472
ζλ Ω		ço,	473 CGCGACGGGGCCTCACAGGCACCTGCAGCACGCTGCGCACCGCGCCTCG 532
දු දු		Å qa	533 TTGCTCATGATCGCGCCGGGGTGCCGTCGGCGTCATCGCCCTCGCGCCGCTGCTC 592
<u>ئ</u> ۾		λό da	593 TTTGGCCGGGCGAGGTGTGCGACGCTCCGGCTCCAGCGGGGGGCGGGAACCC 652
<u>م</u> م		ç d	653 TCCTAIGCGGCTTCTCCACCGGGGGGCCTTCCACCGGCTTGGCGTGGTGCTGTT 712
Sy Dp		Qy Dp	713 GTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTC
RESULT US-10-2	67A-445	<i>&</i> 8	773 CTGCCGTTGCCGGCCACCATGCAGGTGCCAAGGTAAAGGAAGCACCTGATGAGGCT 832

RESULT 10
US-10-225-567A-445
Sequence 445, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences

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CCCCTGATCTATACGGCTTTCAACAAGAACTACAACAGCGCCTTCAAGAACTTCTTTTCT 1062
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Pred. No. 1.1e-129;
0; Mismatches 279; I
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nilarity 70.6%; P
Conservative 0;
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Best Local Similarity
Matches 729; Conserv
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US-10-345-680-39
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GENERAL INVORMATION:

APPLICANT: Millennium Pharmaceuticals Inc.

APPLICANT: Carroll, Joseph M.

APPLICANT: Carroll, Joseph M.

APPLICANT: Healy, Aileen

APPLICANT: Weich, Naileen

APPLICANT: Weich, Naileen

APPLICANT: Weich, Naileen

APPLICANT: Weich, Naileen

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14333, 28059, 7366, 12212,

TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 1847, 1849,

TITLE OF INVENTION: 15513, 17822, 684A, 10217, 897, 1761, 8990 OR 13249 MOLECULES

FILE REFERENCE: MFILO2-019PIRNOWNIN: US/10/352,684A, 1761, 8990 OR 13249 MOLECULES

FILE REFERENCE: WEICH OF SOURCE CORONS OF SOURC
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62553, 302, 323,
2058 OR 6351 MOLECULES.
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Pred. No. 1.1e-129;
0; Mismatches 279; Indels 24;
       CORNERANT: NITOLOGNERS

APPLICANT: Willennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Verkateswarlu, Karicheti
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056;
FILE REFERENCE: MUNENTION: 12303, 985, 13237, 13601, 18926, 318, 2056;
FILE REFERENCE: MUNENTION: 12303, 985, 13237, 13601, 18926, 318, 2056;
FILE REFERENCE: MUNER: US 60/349,511
CURRENT APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-01-18
PRIOR PELING DATE: 2002-02-28
PRIOR PELING DATE: 2002-03-15
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR PELING DATE: 2002-10-21
PRIOR PELING DATE: 2002-11-05
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Best Local Similarity 70.6%;
Matches 729; Conservative (
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US-10-345-680-37
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ORGANISM: Homo Sapiens
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NAME/KEY: CDS
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US-09-823-245A-617

US-09-823-245A-617

Sequence 617, Application US/09823245A

Publication No. US20020039760A1

GENERAL INFORMATION:

APPLICANT: Wong, Gordon G.

APPLICANT: Agostino, Michael J.

APPLICANT: Rentel, Kim

APPLICANT: Rentel, Kim

APPLICANT: Rentel, Kim

APPLICANT: Golve, Kamalakar

APPLICANT: Golve, Kamalakar

APPLICANT: Genetics Institute, Inc.

APPLICANT: Genetics Institute, Inc.

TITLE OF INVENITON: POLYNUCIEOTIDES ENCODING NOVEL SECRETED PROTEINS

FILE REPRENCE: GIN 401

CURRENT FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06
                                                                                                          946 GIGCTCTGCTGGATCCCCTTCTTTCTCACCGAGCTCATCAGTCCCCTCTGCTCCTGTGAC
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GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCC
                                                                              TGGCGGGAGCAGAAGGAGAGCGAGCAGCCATGATGGTGGGAAATTCTGATTGGCGTGTTT
                                                                                                                                                             GIGCIGIGGAICCCCTICTICCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGC
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43.1%; Score 496; DB 13;
Best Local Similarity 70.5%; Pred. No. 4.1e-129;
Matches 728; Conservative 0; Mismatches 280;
                                                                                                                                                                                                                                                                                                                                                                                                             1133 AAGCAGAGATGA 1144
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US-09-823-245A-617
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LENGTH: 2700
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43.2%; Score 497.6; DB 16; Length 1159;
Best Local Similarity 70.6%; Pred. No. 1.1e-129;
Matches 729; Conservative 0; Mismatches 279; Indels 24;
  PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: US 60/392,480
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/394,128
PRIOR APPLICATION NUMBER: US 60/394,128
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-31
PRIOR FILING DATE: 2002-08-13
PRIOR PILING DATE: 2002-08-13
PRIOR PILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-08-13
PRIOR FILING DATE: SO02-08-13
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PRIOR FILING DATE: SO02-08-13
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                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (64)
US-10-352-684A-15
                                                                                                                                                                                                                                                    SEQ ID NO 15
LENGTH: 1159
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                                                                                                                                                           DB 11; Length 1074;
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                                                                                                                                                         Score 492.8; DB 11;
Pred. No. 2.4e-128;
0; Mismatches 282;
                                                                                                                                                         ch 42.8%;
il Similarity 70.3%;
726; Conservative 0
   PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 446
LENGTH: 1074
                                                                                                           sapiens
                                                                                      TYPE: DNA
ORGANISM: Homo
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Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TILLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TILLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION WINBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION WUNBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
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US-09-826-509-446
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us-09-976-782-15.rnpb

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Search completed: September 7, 2004, 18:33:10 Job time : 592 secs
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7, 2004, 14:14:17; Search time 4454 Seconds (without alignments) 11210.412 Million cell updates/sec
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1152
1 cgccatggaggccgctagcc.....aagcagagatgaacacaggg 1152
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		AX527761 Sequence	700	207	: 2	S	orpes 71	AB065453 Homo sapi	AC009404 Homo sapi	AJ308679 Homo sapi	A39678 Sequence 1	X69867 M.musculus	AR080627 Sequence	AX549160 Semishos	AF498985 Homo sapi	AK094255 Homo sapi	AX280823 Sequence	AC128353 Rattus no	AC0/3/33 Mus muscu A74295 Seguence 7	AR038836 Ŝequence	A74289 Sequence 1	AX3328430 Sequence AX392847 Sequence	Z18278 Mus musculu	L10072 Rattus norv	AKUSU628 SEQUENCE AC073744 Mis miscri	AC146825 Otolemur	AX188694 Sequence	AC14672B Otolemur	AJ308680 Homo sapi	A39680 Sequence 3	AS1411 H.Sapiens D G28709 SWSS3980 Rr	Homo sar	AC093726 Homo sapi	Ratt	Seq	Continuation (3 of AC068651 Mus muscu			COOC-MON-15 TAG Tearil	007-001-17 THE TOTAL OF THE TOT			rtohrata	Hominidae;	, Burqess, C.E., Mishra, V.,	.A., Zerhusen, B.D.,	dougall,J., Stone,D.,
SUMMARIES		AX527761	AX301	AX375	AX342	AX526	AX646	AB065	AC009	HSA30	A39678		AR080627	KAISHISB AX549160	AF498985	AK094255	AX280823	AC128353	A74295	AR038836	A74289	AX392847	MM5HT5SE	RATSHTSA	AC073744 0	AC146825	AX188694	AC146728	HSA308680	A39680	G28709	AC074285	AC093726	AC111733	AX188693	AC111011_2 AC068651_	ALIGNMENTS		1152 hp nus	WO0230974.	284		Craniata.	, Catarrhini	Lepley, I		lach, V.,
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Score		1152	1064 8		1060	1016	756.2	756.2	749.8	745	732.8	732.8	729.8	497.6	496	494.4	492.8	488.7	484.4	484.4	424.6	424.6	424.6	416	394.8	378.8	378.2	350.4	348.8	334.4	320	318.4	318.4	316.4	297	273.6		д,		2.						Kek	Z.A.o
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1020

1140

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ATVSFQVSGDSWREQKERRAAMWVGILIGVPFLCWIPPFLTELISPLCACSLPPIWKS
IFLMLGYSNSFRPDLIYTAPNKNYNNAFKSLFTKQR"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Liu,X., Patturajan,M.
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                                                                                                                    TTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG
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GTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGA
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Novel proteins and nucleic acids encoding Patent: WO 0174851-A 9 11-OCT-2001,
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Pred. No. 2.7e-168;
0; Mismatches 0;
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from Patent WO0174851.
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Pred. No. 2.7e-182;
Mismatches 0;
                          same
   Gunther, E. and Bllerman, K.
Proteins and nucleic acids encoding
Patent: WO 0230974-A 15 18-APR-2002;
Curagen Corporation (US)
                                                                                                         /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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121 CGGCGCCGTCCTGCCGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTCC 180	GGCCATCA GGCCATCA GATCGCGC GGCCAGG GGGCCAGG GGGCCAGG GGCCAGG CGCCTTCT	GCCTT AAGAT AAGAT AAGAT AAGAT CCGGC CCGGC TTCAC TTCAC TTCAC	993 ĠĊĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĠĸĸŦĸĠĸŢĸĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸŢĠĸ

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481 GGCCATCACACACACACACACACACACACACACACACACA	LOCUS LO

Db 355 CGTCGGCTGCTGGGCCGGAGCCTGTGCACGTCTCCTTCCACGTG 405 QY 425 CTGTGCTGCCCGCGGCCTCGGGAACGTGGCGGCCATCGCCTGGGCGACGACGACGACGTGGCGGCCATCGCCTGGGCGCCACGGGCCC 484 Db 406 CTGTGCTGCCCGCGGCGCCGTGGCGGCCTTCGCCCTGGGCCGCGACGACGACGACGACGACGACGACGACGACGAC	Oy 545 GCGCTCGCCGGGTGCCGTCGTCGCCCTCGCCCCGCGCTGCT	Oy 605 GAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCTATGCCGC 664		766	Db 820 ACGGCACATTGCAAACGAACGTTCCTTCCAGGGGGAACTTCTGGGGGGAGCGGGAGCGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGGGGAGCGGGGGAGCGGGGGG		Qy 1025 TGGAAAGCATATTTCTGTGGCTACTCCAATTCTTCTACCCCTGATTTAC 1084	AX526745 1155 bp DNA linear bar 21_MoV-200	TION Sequence 29 from Patent W00224733. ION AX526745 ION AX526745.1 GI:25171536 DS	SOURCE unidentified ORGANISM unidentified REFERENCE 1	AUTHORS Mishra, V.S., Spytek, K.A., Taupier, R.J., Vernet, C.A., Colman, S.D., Gorman, L., Tchernev, V.T., Malyankar, U.M., Shenoy, S., Tchernev, V.T., Padigaru, M., Patturajan, M., Burgess, C.E., Smithson, G., Millet, I., Peyman, J.A., Stone, D., Gunther, E. and Rilerman K.	TITLE Human polynucleotides and polypeptides encoded thereby JOURNAL Parent: WO 0224733-A 29 28-MAR-2002; Curagen Corporation (US) FEATURES Location (One) 1:6125	rce
10	Oy 1145 ACACAGGG 1152 Db 1114 ACACAGGG 1121	RESULT 5 AX342670 LOCUS LOCUS DEFINITION Sequence 25 from Patent W00198351. VERSION AX342670 TI19 bp DNA linear PAT 12-JAN-2002 DEFINITION AX342670 VERSION VERSION AX342670.1 GI:18152050	KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 AUTHORS Lal, P., Baughn, M.R., Hafalia, A.J., Nguyen, D.B., Gandhi, A.R., Kallick, D.A., Griffin, J.A., Yue, H., Khan, F.A., Patterson, C., Lu, D.A., Tribouley, C.M., Lu, Y., Walia, N.K., Graul, R., Yao, M.G., Yang, J., Ramkumar, J., Au-Young, J., Hernandez, R., Walsh, R.T. and	BOTOWSKY, W. L. JOURNAL Patent: WO 0198351-A 25 27-DEC-2001; FEATURES Incyte Genomics, Inc. (US) SOURCE I. 1119 HOMO Sariens"	/mol_type="unassigned DNA" /db_xref="taxon:9606" /note="Incyte ID No: 7474977CB1"	92.0%; Score 1060; DB 6; Length 1119; 4; Conservative 0; Mismatches 5; Indels 21; ATGGAGGCGCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGAC	65	Qy 125 GCCGTCCTGCCGGGCCGAAGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTG 184 Db	Qy 185 CTAGHGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGGCTGGTCACCATCCGG 244	Qy 245 CGGGTCCGTGCCTTCCACCGCGTGCCCCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC 304	Qy 305 GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCTGGCGAGTGAGCTGTCGACCGGGCGA 364 Db 295 GAACTAGTGGCAGCGTGGCGATGCCACCGAGCTGGCGAGTGAGCTGTCGACCGGGCGA 354	Qy 365 CGTCGGCTGCTGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424

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FGRGEVCDALUQRCQVSREPSYAAFSTRGAFHLPLGVVPFVYRKIYEAAKFRFGRRRR
AVLPLPATMQVRGGLRNVAMGKRLLEKEAASRMGEWAEACTNGARAQRSPGAHEDKFA
ISSSEAGTEGLVVTGSPGTQVRGSPAAYLVRAEERVSQSAR"
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TCCAATTCTTTCTACAACCCCCTGATTTACACAGCTTTTTAACAAGAACTACAATGCC
                                                       Gaps
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Pred. No. 2.1e-116;
0; Mismatches 13;
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/db_xref="reaxon:9606"
join[2011. 277,1118. 2192,2218.
/note="unnamed protein product"
                                                                                                               TTCAAGAGCCTCTTTACTAAGCAGAGATGAACACAGGG
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Sequence 609 from Patent EP1270724.
AX646417
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            /db xref="taxon:32644"
/noTe="Description of Unknown Organism: NOVX Nucleic Acid"
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from the whole human genome sequences using our automated
                     system that contains programs of gene finding (GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.

And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="seven transmembrane helix receptor"
/evidence=not_experimental
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Pred. No. 1.2e-116;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                        1. .44312
/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="CBRC7TM_16"
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/chromosome="2"
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Direct Submission

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Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,

Tel:81.3-3599-8080, Fax:81-3-3599-8081)

This sequence is a seven transmembrane helix receptor candidate
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (07-OCT-2000) Department of Genetics, Mashington
Submitted (07-OCT-2000) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 7, 2000 this sequence version replaced gi:9454621.
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44 (bases 1 to 112883)
Waterston, R. H.
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Submitted (26-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                     CTIGGCGIGGIGCCGITIGICIACCGGAAGAICTACGAGGCGGCCAAGITICGTTICGGC
                                                                               CGCCGCCGGAGAGCTGTGCTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG
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Homo sapiens BAC clone RP11-28H22 from 2, complete sequence.
AC009404
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Center code: WUGSC
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Direct Submission
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatanes, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are polymorphic base pair differences in the overlaps between the clones RPI1-425F6, RPI1-28H22, and RPI1-425F6. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                           Ap; the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence RP11-28H22 contains imperfect dinucleotide (CT and GC repeats from base position 53407 to 53507. The region is covered by a single clone; the fidelity of the sequence cannot be guaranteed. The length of sequence is consistent with PCR from clone DNA, and corresponds to restriction digest information: hindIII band size 5664 in silico, and 5694 real.
                                                                                                                                                                                                                                                                                                                                                                                                      The clone sequenced to the left is RP11-425F6, 200 bp overlap, clone sequenced to the right is RP11-98C1, 200 bp overlap. Act start of this clone is at base position 157644 of RP11-425F6; actual end is at base position 21685 of RP11-98C1.
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. L MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST AW892944 (NID:g8057149)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NID:97855185)"
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NEIGHBORING SEQUENCE INFORMATION:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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/rpt_family="MER1_type"
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/rpt_family="MER1_type"
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/note="similar to
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/note="similar to
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/note="similar to
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/note="similar to
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'note="similar to
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/note="similar to
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/note="similar to
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/note="similar to
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                                                                                                                                       SOURCE INFORMATION:
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center project name: H_NH0028H22

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Qy 1 CGCCATGGAGGCCGC	Db 41796 cGCCATGGAGGCCGC	Qy 61 CGAGACCAGCAGC-C	Db 41856 CGAGACCAGCAGCA	2y 120 GCGCCCGTCCTGC	Db 41916 GCGGCCGTCCTGC	QY 180 CGCTGCTAGTGCTGC	Db 41976 CGCTGCTAGTGCTGC	Qy 240 TCCCGCGGGTCCGTC	Db 42036 TCCCGCGGGGTCCGTC	Qy 300 CGGACGAACTAGTGC	Db 42096 CGGACGAACTAGTGC	Qy 360 GGCGACGTCGGCTGC	Db 42156 GGCGACGTCGGCTGC	Qy 420 CCTGT	Db 42216 CCTGTGCCACGTGTG	Qy 455 GCGCCATCGCCCTG	Db 42276 GCGGCCATGGCCTG	Qy 515 ACCGCAGCGGGC		QY 575 GCCTCGCGCTG	Db 42396 GCCCTCGCGCCGCTG	Qy 635 CAGGTGAGCCGGGAA	Db 42456 CAGGTGAGCCGGGAA	Qy 695 CTTGGCGTGCTG	Db 42516 CTTGGCGTGGTGCCC	Qy 755 CGCCGCCGGAGAGCT	Db 42576 CGCCGCGGAGAGCT	Qy 815 GAAGCACCT 823	Db 42636 AACGTTGCT 42644	638	DEFINITION HOME SADDIES	ACCESSION ACO11638 ACT.71	S HTG: HTGS PF HOMO SADIENS ISM HOMO SADIENS FURATYOTA: N	cannot innotaning
repeat_region 28262976 /rpt_family="MER1_type" misc_feature 35343669	Φ	e)	υ	ρ	· o	و د) ,) (ט מ) q	// // // // // // // // // // // // //) <u>a</u>	/note=	و د	٠ () 9) a	و د	ט פ) g		ט ס) 9	feature	feature	feature 4	Feature) q	 ه ر	/note="	/note= n 5025.	Query Match 65.6%; Score 756.2; DB 9; Length 112883; Best Local Similarity 95.4%; Pred. No. 1e-116; Matches 810; Conservative 0; Mismatches 13; Indels 26; Gaps 2;	

SCCGGGCCGAGGCCCCTTCTCTCTCTCACGGTCCTGGTGGTGT 179 41855 SCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGCTGGTTCCGGTCACCA 42035 TGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCT 299 CCTCGTTGCTCATGAGGCTCGCCGGGGTGCCGTCGGCGCTCATC 574 AACCTCCTATGCCGCCTTCTCCACCGGGGGCGCTTCCACCTGCCG 694 3CTGGGCCGGAGCCTGTGCCACGTGGGATCTCCTTCCACGCCGGAG 419 GGAICTCCTICCACGGCTGTGCTGCCCGGCCGGCCTCGGGAACGTG 42275 42575 184328 bp DNA linear HTG 01-MAR-2000 one RP11-13G16, *** SEQUENCING IN PROGRESS ***, 55 239 119 GCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCG 359 GGGCCGCGACGGGCCATCACACGCCACCTGCAGCACACGCTGCGC 514 TIGIGCTGCCGTTGCCGGCCACCATGCAGGTCCAAGGTCAAAG 814 ------CTGTGCTGCCCGCGGGCTCGGGAACGTG 454 GCTCTTTGGCCGGGGGAGGTGTGCGACGCTCGGCTCCAGCGCTGC 634 GETTIGICIACCGGAAGAICTACGAGGCGGCCAAGITTCGTTTCGGC 754 09 Homo sapiens Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; GCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACC SCTGATCGCTGCCACTTTCCTGGAACCTGCTGGTTCCGGTCACCA SCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACC -GGACCCGGGACCCCAAGCCCCGAGGGATACTCGGTTCGACCCCGA GTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTCGCC 7137674 SOURCE ORGANISM

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3 of 1662 bp in length
f 100 bp
g of 2426 bp in length
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g of 2736 bp in length
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of 1563 bp in length
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of 3405 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (Masor-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Max 1, 2000 this sequence version replaced gi:6957833.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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------ Project Information
Center project name: L3324
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                    1 (bases 1 to 184328)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-13G16
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COMMENT

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* 146707 154091: contig of 7385 bp in length * 154092 154191: gap of 100 bp * 154192 163194: contig of 9103 bp in length * 163295 163394: gap of 100 bp * 163395 173882: contig of 10488 bp in length * 173883 173882: gap of 100 bp * 173883 173882: gap of 100 bp * 173893 173823: contig of 10346 bp in length. * 173983 184328: contig of 10346 bp in length. 1.184328 1	misc_feature /clone_lib="RPCI-11 Human Male BAC" 1.1382	sc_feature sc_feature sc_feature sc_feature	misc_feature 999011351 /	misc_feature 16144. 17521	QY 1 CGCCATGGAGCCGCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACC 60 Db 106221 CGCCATGGAGCCGTTACAGTGGCCACCGCCGGCGGTTGCCCTTGCCTTGGACC 106280 QY 61 CGAGACCAGCAGCCGGAACCCCAAGCCCGAGAGAATACTCGGTTCGACCCCGA 119 Db 106281 CGAGACCAGCAGCAGGACCCCAAGCCCGAGAGGATACTCGGTTCGACCCCGA 106340 QY 120 GCGGCCGCCAGCAGAGACCCCAAGCCCCAAGAGCCCGAAGAGGATTCTCACCCCCA 106340 QY 120 GCGGCGCCCTCTCTGCCGGGACCGAGAGGCCGCACCGACAGGATTCTCTGATCAGATGCTTCGATGATA 179	Db 106341 GGGGGGCGTCTGGCGGGGGGGCCCTTTGTTTTTTTTTT

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PATENT: WA 9418319-94 1 18-AUG-1994;
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Other publication CA 2153162 940818
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Other publication PB 806244T 960709.
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Pred. No. 1.9e-114;
0; Mismatches 20;
                                                      /codon_start=1
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/db_xref="PSEUDO:CAC36299.1"
/db_xref="REMTREMBL:CAC36299"
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/gene="5-HT5B"
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       gene="5-HT5B"
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AUTHORS Matthes, H. TITLE Direct Submitted (18-DEC-1992) H. Matthes, Laboratoire de Genetique Moleculaire des, Eucaryotes, Departement de Neurobiologie, 11 rue Humann, F-67000 Strasbourg, FRANCE Humann, F-67000 Strasbourg, FRANCE Location/Qualifiere 1. 2061	IFLWLGYSNSFENPLIYTAFNKNYNNAFKSLFTKQR" 3121088	Query Match 83.6%; Score 732.8; DB 10; Length 2061; Best Local Similarity 79.9%; Pred. No. 1.8e-112; Matches 911; Conservative 0; Mismatches 202; Indels 27; Gaps 5 ATGGAGGCGGTAGCCTTTCAGTGGCCACCGCGGGGTTGCCCTTGCCCTGGGACCCGAG 11	65 372 125 426 185	Db 486 CTGGTGTTGCTGATCGCACTTTCTTATGGAATCTGGTGGTTCTGGTGACTATCTG 545 Oy 245 CGGGTCCGTGCCTTCCACCGCATAACTTGGTGCCTCGACGGCTGTCCGACG Db 546 CGGGTCCGCGCTTCCACCGCTGCCACATAACTTGGTGCCTCCGACGCTCTCGGAT 605 Oy 305 GAACTAGTGGCAGCGTTGCCACACACACACACACACACCGTCTCGGAT 605 Oy 305 GAACTAGTGGCAGCGCTGGCGACACACACACACACACACA
	Qy 785 GCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTC 844 Db 1077 GCCACCACGCAGGCAAAGGAAGCACCTCCGGAGTCTGAGGATGTTC 1124 Qy 845 ACGGCACATTGCAAAGCAACGACGTCCTTCCAGGAGCGCGGGAGCAG 904 Db 1125 ACAGCCGTCCCGGAGCACATTACCAAGCAACAGTAACTTCCAGGAGAACTCCTTGCCGGAGAGCAG 1184	905 AAGGAGGAGCAGCATGATGGTGGGAATTCTGATTGGCGTGTTTGGCTGGC	OY 1025 TGGAAAGCATATTCTGTGGCTTGGCTACTCCAATTCTTCAACCCCTGATTTC 1084	MASHTSBR MASHTSBR 2061 bp mRNA linear ROD 26-MAY-1993 LOCUS LOCUS MASHTSBR MASHTSBR 2061 bp mRNA linear ROD 26-MAY-1993 ACEDSION VERSION VERSION S.69867.1 GI:288735 S-HTSB serotonin receptor. S-HTSB serotonin receptor. S-HTSB serotonin receptor. S-HTSB serotonin seconds Musculus (house mouse) Nusculus (house mouse) REFERENCE ORGANISM Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus. REFERENCE I (bases 1 to 2061) AUTHORS Muscatelli,F., Martei,M.G. and Hen,R. Muscatelli,F., Martei,M.G. and Hen,R. TITLE Muscatelli,F., Martei,M.G. and S-Hydroxytryptamine5B receptors define a new family of serotonin receptors: cloning, functional JOURNAL Mol. Phasmacol. 43 (3), 313-319 (1993) REFERENCE 2 (bases 1 to 2061) REFERENCE 2 (bases 1 to 2061)

QY 123 GCGCCGTCCTGCCGGGCCGAGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGGCGC 182	Oy 183 TGCTAGTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCC 242	243 COCGGGGCCGTCCACCACCACCACATACTTCACTACGCCTCGACGCCCTCGG 30	535 TGCGCGTCCGCGCTTCCACCGTGTGCCACATAACTTGGTAGCCTCGACCGCCGTCTCGG 59	QY 303 ACGAACTAGTGGCAGCGCGATGCCACCGAGCCTGGCCAGTGACCTGTCGACCGGCC 362 Db 595 ACGTCCTGGTGGCGGCTCTGGTGATGCCACTGAGCCTGGTGAGCGTGTCGGCTGGGC 654	363 GACGT 655 GACGT	423	Qy 483 CCATCACAGGAACTGCAGCAGCAGCAGCAGCCGCGCCTCGTTGCTCATGA 542	Qy 543 TGGGGCTGGCCGGGTGCGTGGCTCATCGCCCTCGCGCCGCTGCTCTTTGGCCGG 602 bb 826 TGGCGATCACCTGGCGCACTGTCGCCCTCATCGCGCTCGCT	Qy 603 GCGAGGTGTGCGACCTCCGCTCCAGCTGAGCCGGGAACCCTCCTATGCCG 662 Db 886 GCGAAGCCTACGATGCTCGGCTTCCCAGGTGAGCCAGGAGCCTTCGTACGTG 945	QY 663 CCTICTCCACCGGGGCCTTCCACCTGCGGCTTGGCGTGGCG	QY 723 AGATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCAGAGCTGTGCTGCCGTTGC 782 IIII	1066 CCGCCACCACCACCACCACCACCACCACAGGAAGGAAGCACCTCAGGAGTCTGAGGACCGGTT 1 843 TCACGGCACATTGCAAAGGAACGGTGTCCTTCCAGGTGAGCGGGGACCACTCCTGGCGGGAGC 9	1114 TCACCGCGCGTTCCAGAGCGACAGTGGCCTTCCAGACAAGTGGAGACTCCTGGCGGGAGC 1	OY 903 AGAAGAGAGAGCAGCCATGATGGTGGAAATTCTGATTGGCGTGTTTGTGCTGTTTTTGTT 962	gy 963 GGATCCCCTTCTTCCTGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCA 1022 Db 1234 GGATCCCCTTCTTCCTGACGAGCTCGTCAGCCCTCTGCGCCTGCAGCCTCCACCCA 1293	Qy 1023 TCTGGAAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTCTTCACCCCCTGATTT 1082	1083 ACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGGAGAGAT 114	Db 1354 ACACGGCCTTTAATAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGT 1413 Qy 1143 GAAÇA 1147	Db 1414 AAGCA 1418
Qy 545 GGGTTGGCCGGGGGGTCGGCGCTCATCGCCCTGCTGCTGTTGGCGGGGGC 604 Db 837 GCGATCACCTGGGGACACTGTCCGCGCTCATTGCTCTCGCCCGCTGCTTTTTGGCTGGGGG 896	605 GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGGGGGGG	0 6	957 TTCTCCACCTGCGGAGCCTTCTACCTGCCTCTAGCGGTGGTCTTCGTCTTCGTCTACTGGAAA 10	QY 725 ATCTACGAGGCCAAGTTTCGTTTCGCCGCGGAGAGCTGTGCGCGTGCCGTTGCC 784 Db 1017 ATATACAAACCGCCAAGTTTCGTTCTGGTCCCAGACGCGGCGGTGCTACCGCTTCCT 1076	785 GCCACCATGCAGGTGAGGTACGTAAAGGAAGGACGTGATGAGGCTGAAGTGTGTTC 8	845 ACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG	Qy 905 AAGGAGAGCGAGCATGATGGTGGAAATTCTGATTGGCGTGTTTGTGCTGCTGG 964	QY 965 ATCCCCTTCTTCCTGAACTCATCAGCCCACTCTGTGCCTGCC	OY 1025 TGGAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTCAACCCCCTGATTTAC 1084	Qy 1085 ACAGCTTTTAACAAGAACTACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGATGA 1144	RESULT 14 AR086627 LOCUS AR080627 2226 bp DNA linear PAT 31-AUG-2000 DEFINITION Sequence 1 from patent US 5968817.	AR080627 GI:1000735	_	AUTHORS Sutcliffe TITLE DNA encod JOURNAL Patent: U	FEATURES Location/Qualifiers Source 1.0.2226 /organ="unknown" /mol_type="unassigned DNA"	ORIGIN Query Match 63.4%; Score 729.8; DB 6; Length 2226; Best Local Similarity 79.6%; Pred. No. 5.5e-112;	911; Conservative 0; Mismatches 207; Indels 27; 3 ccargeaggccgcragccrrrcagragccaccgccggcgrrrcagragccrrggc	301 CAAIGGAAGICICIAACCICICAGGCGCCACCCCIGGCAIIGCCIIICCICCGGGACCCG	Qy 63 AGACCAGCAGCGGACCCCAAGCCCGAGAGGATACTCGGTTGACCCCGAGGG 122

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GRFYVPLAVVLFVYWKIYXVARKFRFGRRRRAVVPLPATTQAKEAPQESETVFTARCR
ATVAPCYISGDSWREGKERRAMMYGTLIGVPVLCWIPPFLTELVSPLCRCSLPPIWKS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Location/Qualifiers
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                                                                                                                                                                                                                                                      Exhander, M. G., Lovenberg, T.W., Baron, B.M., Lecca, L.,
Barlander, M. G., Lovenberg, T.W., Baron, B.M., Lecca, L.,
Cannon, R., Burns, J.E. and Sutcliffe, G.J. Siegel, B.W., Foye, P.E.,
Two members of a distinct subfamily of 5-hydroxytryptamine
receptors differentially expressed in rat brain
Proc. Natl. Acad. Scl. U.S.A. 90 (8), 3452-3456 (1993)
                                        RATSHTSB 2240 bp mRNA linear ROD Rattus norvegicus 5-hydroxytryptamine receptor (5HTSb) m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 729.8; DB 10; Length 2240;
Pred. No. 5.5e-112;
0; Mismatches 207; Indels 27;
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note="putative"
                                                                                                                                        5-hydroxytryptamine receptor; serotonin receptor
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'function="unknown effector coupling'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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'protein id="AAA40616.1"
'db xref="GI:310075"
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103. .1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
'label=5-HT5b
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                                                                                                                   GI:310074
                                                                                                                                                                              Rattus norvegicus
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APPLICANT: Erlander, Mark G
APPLICANT: Erlander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
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US-09-018-351-6
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US-09-341-446B-10
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US-08-157-185-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR5099P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08031538
Patent No. 5968817
GENERAL INFORMATION:
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TELEPHONE: 619-554-2937
TELEPAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
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Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Se
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                            OM nucleic - protein search, using frame_plus_n2p model
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US-08-356-405-2
US-08-356-405-9
US-08-31-538-4
US-08-461-812-4
US-08-157-185-15
US-09-850-790A-15
US-09-332-837-15
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US-07-817-920-6
US-08-117-006-6
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Result No.

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                                                                                        904
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APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: How, Rene
APPLICANT: How, Rene
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for These
TITLE OF INVENTION: Polypeptides and Uses Thereof
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie R
REGISTRATION NUMBER: 38,619
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Rhone-Poulenc Rorer Inc.: 500 Arcola Road, 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08356405 Patent No. 5807691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (610)454-3839
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-356-405-2
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295
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                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                     US-09-976-782-15 (1-1152) x US-08-031-538-2 (1-370)
                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                    Gaps:
                                                                                                                                          1.24e-92
1444.50
82.85%
77.84%
67.06%
                  LENGTH: 370 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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     SEQUENCE CHARACTERISTICS
                                                                       , MOLECULE TYPE: protein US-08-031-538-2
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                               Alignment Scores:
Pred. No.:
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                                                         318 IleTrpLysSerIlePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle 337
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APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
APPLICANT: Plassat, Jean-Luc
APPLICANT: Plassat, Gent-Luc
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (SHTSA), Nucleic Acids Coding for These
TITLE OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||||
8 ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATPLICATION NUMBER: PC 92/08081
FILING DATE: 01-JUL-1992
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                       3: Rhone-Poulenc Rorer Inc.
500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     Sequence 9, Application US/08356405
Patent No. 5807691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38,619
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (610)454 - 3839
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71.31%
61.00%
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                          Collegeville
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ZIP: 194
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259 PheThrAlaArg---HisAlaThrValThrPheGlnThrGluGlyAspThrTrpArgGlu 277
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   37
93
11
   Conservative:
               Mismatches:
Indels:
Gaps:
                                                                                US-09-976-782-15 (1-1152) x US-08-356-405-2 (1-357)
71.118
60.838
47.478
Percent Similarity:
Best Local Similarity:
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US-08-031-538-4
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                LeuGlyPheLeuValAlaAlaThrPheAlaTrpAsnLeuLeuValLeuAlaThrIleLeu 66
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CTAGTGCTGCTGCCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG
                                                                    GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA
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                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office ADDRESSEE: Patent Counsel STREET: 10666 No. 5968817th Torrey Pines Road, TPC
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HUMAN SEROTONIN RECEPTORS, DNA THE RECEPTORS, AND USES THEREOF
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Mismatches:
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                                                                                                                                                                                                                                                                            ACTION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIPICATION NUMBER: US/08/031,538
ATTORNEY/AGENT INPORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR5099P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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71.278
60.858
47.108
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AMINO ACID
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                                                                                                                                                              ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity:
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Sutcliffe, J Gregor Erlander, Mark G Lovenberg, Timothy W

APPLICANT: APPLICANT: I

Sequence 4, Application US/08031538 Patent No. 5968817 GENERAL INFORMATION:

US-08-031-538-4

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------TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu
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Matches:
Conservative:
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   28,678
ER: 36536-B/JPW/MAT
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REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 3651
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2122780400
TELEPHONE: 213910525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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448.00
48.35$
32.32$
20.80$
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TOPOLOGY: linear
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         CAGCACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCGGGTG 559
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                                                                                                                        560 CCGTCGGCGCTCATCGCCCTCGCGCCCTGCTTTGCCCGGGGCGAGGTGTGCGACGTT
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APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING HUMAN 5-HTID RECEPTORS AND TITLE OF INVENTION: USES THEREOF
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .097 AAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
^^TWARE: PatentIn Release #1.0, Version #1.30
-^*TON DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08461812
Patent No. 5935925
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
: U.S.A.
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STATE: New York
COUNTRY: U.S.A.
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102 ValMetPro-----IleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGln 119
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216 AlaPheTyrPheProThrLeuLeuLeuIleAlaLeuTyrGlyArgIleTyrValGluAla 235
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------TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu 61
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                                                                                                                                                                                                                                                         30 SerGlnAsnCysSerAlaLysAspTyrIleTyrGlnAspSerIleSerLeuPro---
             390
127
63
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56
             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                              US-09-976-782-15 (1-1152) x US-08-157-185-15 (1-390)
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             1.43e-23
448.00
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                                               Percent Similarity:
Best Local Similarity:
 Alignment Scores:
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                                 CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG 814
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AspvalProSerGluSerGlySerProValTyrValAsnGlnValLysValArgValSer
                                                                                                                                                              GAGAGG
                                                                                                 GAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bard A. Jonathan
APPLICANT: Branchek A. Theresa
APPLICANT: Meinshank L. Richard
TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN
TITLE OF INVENTION: RECEPTOR (5-HT4B) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                        1088 GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                              41908-A-PCT-US/JPW/MAT
                                                                                                                                                                872 TTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAGAAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION UNDER:
FILING DATE: 15-JUN-1995
CLASSIFICATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08157185
Patent No. 5985585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White P., John
REGISTRATION NUMBER: 28.678
REFRENCE/DOCKET NUMBER: 41908
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
INPORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-157-185-15
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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Oy 314 CGAGCAGCCATGATGGTGATTTTGGCGTGTTTGTGCTGGATCCCCTTC 973 ::: ::: :::	1088	RESULT 7 US-08-281-526B-15 Sequence 15, Application US/08281526B Sequence 15, Application US/08281526B Sequence 15, Application US/08281526B GENERAL INFORMATION: APPLICANT: Branchek A. Theresa APPLICANT: Weinshank L. Richard TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN	ILLE OF INVESTICAN: TACCETION: (S-H14B) AND USES INDRESOR NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A.	COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/281,526B	FILING DATE: 27-JUL-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: White P., John REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 41908-1/JPW TELECOMUNICATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525 INFORMATION: FOR SEQ ID NO: 15:	Supplement Constraints Supplement Supp	Pred. No.: 1.43e-23 Length: 390 Score: 448.00 Matches: 127 Score: 448.00 Conservative: 63 Bert Local Similarity: 48.32\$ Mismatches: 147 Query Match: 20.80\$ Indels: 56 DB: 3 Gaps: 13 US-09-976-782-15 (1-1152) x US-08-281-526B-15 (1-390) QY 59 CCGAGACCAGCAGCAGAGCCCAAGCCCGAGAGGATACTCGGTTCGACCCCG 118

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974 TTCCTGACGGAACTCATCAGCCCACTCTGT-----GCCTGCAGCCTGCCCCCCCTTTGG 1027
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               TCGGCGCTCATCGCCCCTCGCGCCGCTGCTTTTGGCCGGGGCGAGGTGTGCGACGCTCGG 622
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Sequence 15, Application US/09332837

Sequence 15, Application US/09332837

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan

APPLICANT: Branchek, Theresa

APPLICANT: Weinshank, Richard

TITLE OF INVENTION: Methods of Obtaining Pharmaceutical Compositions

FILE REPERENCE: 1990-06-14

CURRENT APPLICATION NUMBER: US/09/332,837

CURRENT FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 390
                                  ------GGCCGCCGC---CGGAGAGCTGTG
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                                                                        ### Sequence 15, Application US/09450790A

| Sequence 15, Application US/09450790A
| Sequence 15, Application US/09450790A
| Sequence 15, Application US/09450790A
| Sequence 15, Application Sequence 15, Application: Barachek, Theresa APPLICANT: Barachek, Theresa APPLICANT: Weinshank, Richard L
| TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN RECEPTOR (SHT4B) AND USES THEREOF FILE REFERENCE: 1795/419081A
| CURRENT PLING DATE: 1999-11-29
| PRIOR APPLICATION NUMBER: 08/281,526
| PRIOR APPLICATION NUMBER: 09/291,690
| PRIOR APPLICATION NUMBER: 07/971,690
| PRIOR FILING DATE: 1992-11-03
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SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 390
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Patent No. 6475746
GENERAL INFORMATION:
APPLICANT: Weinshank et al, Richard L.
TITLE OF INVENTION: Method of Obtaining A C.
TITLE OF INVENTION: Selective Compound
FILE REFERENCE: 36536-BA
CURRENT APPLICATION NUMBER: US/09/371,705
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 5,935,925
PRIOR FILING DATE: 1999-08-10
PRIOR FILING DATE: 1999-08-10
SOFTWARE: PatentIn Ver. 2.1
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09-976-782-15 (1-1152) x US-09-332-837-15 (1-390)
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                      28,678
---- 1795/39318
           ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEFROM: 212-64-0525
TELEFAX: 212-64-0525
TELEFAX: 212-64-0525
TELEFAX: 310-071-0950
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: AMINO ACID
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433.00
47.84%
31.55%
                                                                                                                                                                                                                                                                              N-terminal
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Best Local Similarity:
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CLONE: 5-HT1DB
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FRAGMENT TYPE:
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DB:
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|31 PhellelleSerLeuValMetProlleCysLysAspAlaCysTrpPheHisLeuAlalle 350
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-----AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGluArg
TyrserAlaLysArgThrProLysArgAlaAlaValMetIleAlaLeuValTrpValPhe
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/817,920
FILING DATE: 19920108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weinshank, Richard L
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R
TITLE OF INVENTION: DNA ENCODING A
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/07817920 Patent No. 5360735 GENERAL INFORMATION:
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New York
COUNTRY: USA
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STREET: 30
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                             Mismatches:
                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                       1.56e-22
433.00
47.84%
31.55%
20.10%
TELEFAX: 212-664-0525
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acids
                                                                                                                                                                                              N-terminal
                                                                                     TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                             STAGES TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AGC------
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: 5-HT1DB
                                                                                                                                                                            NO
                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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|331 PhelleSerLeuValMetProlleCysLysAspAlaCysTrpPheHisLeuAlalle 350
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                                                                                                                                            -----GGCCGCCGC---CGGAGAGCTGTG 772
                                                                                                                                                                             236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln 255
                                                                                                                                                                                                                 --CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG 814
                                                                                                                                                                                                                                                  256 LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
                                                                                                                                                                                                                                                                                       815 GAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC 871
                                                                                                                                                                                                                                                                                                                        276 AspValProSerGluSerGlySerProvalTyrValAsnGlnValLysValArgValSer 295
                                                                                                                                                                                                                                                                                                                                                             -GAGAGG 913
                                                                                              ||||||::: ||||
| AlaPheTyrPheProThrLeuLeuLeuIleAlaLeuTyrGlyArgIleTyrValGluAla
   CTCCAGGGCTGCCAGGTGAGCCGGGAACCC---TCCTATGCCGCCTTCTCCACCCGCGGC
                         GCCTTCCACCTGCCGCTTGGCGTGCTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTIF RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           872 TTCCAGGTGAGCGGGACTCCTGGCGGGGCAGAG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect, Version i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08117006
Patent No. 5639652
GENERAL INFORMATION:
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STREET: 30 Rockefeller Plaza
CITY: New York
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216 AlaPheTyrPheProThrLeuLeuLeulleAlaLeuTyrGlyArglleTyrValGluAla
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124
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                   Matches:
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31.55%
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                        MOLECULE TYPE: protein HYPOTHETICAL: NO
linear
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Best Local Similarity:
                                                                                                                                                       5-HT1DB
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                                                                         ANTI-SENSE: NO FRAGMENT TYPE:
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TOPOLOGY:
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                                                                                                                                                       CLONE:
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----AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGluArg 310
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                        GGCCGCCGC - - - CGGAGAGCTGTG
                                                                      236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln
                                                                                                                         ---CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG
                                                                                                                                                                                                                                                                              276 AspValProSerGluSerGlySerProValTyrValAsnGlnValLysValArgValSer
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Patent No. 565213
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTIF RECEPTOR
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REBERBROEL/DOCKET NUMBER: 1195/
TELECOMMINICATION INFORMATION:
TELEPACNE: 212-977-9550
TELEPACNE: 212-977-9550
TELEPACNE: 212-977-9550
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: unknown
                        740 AAGTTTCGTTTC-
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US-08-216-594-6
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                                                   Percent Similarity:
Best Local Similarity:
               Alignment Scores:
Pred. No.:
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--------AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGluArg 310
                           871
                                                                             GAGAGG 913
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                                                                                                                                                                                                            331 PheIleIleSerLeuValMetProIleCysLysAspAlaCysTrpPheHisLeuAlaIle 350
LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
                          GAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC
                                                 AspValProSerGluSerGlySerProValTyrValAsnGlnValLysValArgValSer
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DAS ENCODING A HUMAN 5-HTIP RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                          1088 GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                           872 TTCCAGGTGAGCGGGACTCCTGGCGGGAGCAGAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WMBER: PCT/US93/00149
FILING DATE: 19930108
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: White, John PREJETRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-64-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISCICS:
LENGTH: 390 amino acids
                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application PC/TUS9300149 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IMMEDIATE SOURCE;
; CLONE: 5-HT1DB
PCT-US93-00149-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 CGCGTGCCGCATAACTTGGTGGCCTCGACGCCGTCTCGGACGACGACTAGTGGCAGCGCTG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 GCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGCTGGGCCGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ValvalCysAspPheTrpLeuSerSerAsp-----IleThrCysCysThrAlaSer 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCCGGGTGCCG 562
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                                                                                                                                                                                                                                                                                            ----TrpLysValLeuLeuValMetLeuLeuAlaLeuThrLeu 61
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| AlaPheTyrPheProThrLeuLeuLeuIleAlaLeuTyrGlyArgIleTyrValGluAla
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236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln
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                                                                                                                                                                                                                                                                                                                                                                                                                      30 SerGlnAsnCysSerAlaLysAspTyrIleTyrGlnAspSerIleSerLeuPro---
  390
124
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149
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Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                               US-09-976-782-15 (1-1152) x PCT-US93-00149-6 (1-390)
                                                                                                                 Indels:
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Conservative: 64 Conservative: 64	203 GCCACTTTCCTGTGGAA 203 GCCACTTTCTGTGGAA 263 CGCTGCCGCATAACTT 323 GCGTGCCACAACTT 323 GCGTGCCACAGGCCT 323 GCGTGCCACGAGCCT 323 AGCTTGTGCCACGTGTC 320 ValvalCyaAspPheft	. 443 137 503 157 157	Oy 623 CTCCAGCGCCAGCTGACCCGCAACCCTCCTATGCCGCCTTCTCCACCCGCGCG 679 :::	Qy 815 GAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC 871 Db :::
JeumetalaAlaArgGluArg	Db Oy Streckpror and Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy	55 CY CY CY CY CY CY	46 46 46 46 46 46 46 46 46 46 46 46 46 4	9.7 Db Db 3.98 Db Db Db Db Db Db Db Db Db Db Db Db Db
	SSULT 15 Sequence 6, Application US/08370542 Sequence 6, Application US/08370542 Sequence 6, Application US/08370542 GENERAL INFORMATION: APPLICANT: Weinshank, Richard L. APPLICANT: Branchek, Theresa APPLICANT: Branchek, Theresa APPLICANT: Harig, Paul R. TITLE OF INVENTION: DISS THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSES: COOPER & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York	FORM: Oppy C com E PC LID R LID R N DAT ER: 435		i STRANDENESS: unknown TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO HYPOTHETIC

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311 LysAlaThrLysThrLeuGlyIleIleLeuGlyAlaPheIleValCysTrpLeuProPhe 330
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CTGG		alle
CCATCTG		enAl
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BCCTG		rpPhe
GCCTGCAGCCTGCCCCCCATCTGC	<u>-</u>	CysT
000	=	spAla
-		LysA
ACTCTGTG	=	lecys
CCAC	=	Prol
rcAGC		a]Met
CTCAT	=	LeuVa
GGAA		eser
974 ITCCTGACGGAACTCATCAGCCCACTCTGT-	::	331 PheileileSerLeuValMetProlleCysLysAspAlaCysTrpPheHisLeuAlaile 350
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Search completed: August 31, 2004, 20:24:14 Job time : 47 secs

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mus musculu rattus norv mus musculu heliothis v homo sapien sta rattus norv oryctolagus cavia porce cavia porce homo sapien didelphis m

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pan troglod mus musculu

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balanus amp pan troglod homo sapien rattus norv

Q9n2b6 P28566 P32305

locusta mig locusta mig

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Searched:

P30940 rattus norv O42385 fugu rubrip P32304 mus musculu

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Run on:

Sequence:

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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
5-hydroxytryptamine 5B receptor (5-HT-5B) (Serotonin receptor) (MR22).
HTRSB OR SHT5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93224515; PubMed=7682702;
Erlander M.G., Lovenberg T.W., Baron B.M., de Lecea L.,
Danielson P.E., Racke M., Slone A.L., Siegel B.W., Foye P.E.,
Cannon K., Burns J.E., Sutcliffe G.J.;
"Two members of a distinct subfamily of 5-hydroxytryptamine receptors
differentially expressed in rat brain.";
Proc. Natl. Acad. Sci. U.S.A. 90:3452-3456(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diet. 333:25-31(1993).

PUNCTION: This is one of the several different receptors for 5-punctions. This is one of the biogenic hormone that functions by Adroxytrypteamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins. Probably involved in surviety and depression.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Brain; in the CAl region of hippocampus, the medial habenula, and rappe nuclei.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

STRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=94039744; PubMed=8224165;
Misden W., Parker E.M., Mahle C.D., Grisel D.A., Nowak H.P.,
Vocca F.D., Felder C.C., Seeburg P.H., Voigt M.M.;
"Cloning and characterization of the rat 5-HT5B receptor. Evidence
that the 5-HT5B receptor couples to a G protein in mammalian cell
                                                                                                                                                                                                                                                                                                                                                                        PRT; 370 AA
                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                    5HID RABIT
SH7 GAVPO
SH1F CAVPO
SH1F HUMAN
SH1F DIDMA
SH1F PAUTR
SH1F MOUSE
GREZ BALLAM
SH1E PANTR
SH1E PANTR
                                                                                                                                                                                                                                    5H7 RAT
OAR1 LOCMI
OAR2 LOCMI
                                                                                                                                                                                                                                                                    SH1F_RAT
SH1A_FUGRU
                                                      5H1A_RAT
5H1D_MOUSE
                                                                SHID_MOUSE
SHT_HELVI
SHT_HUMAN
SHT_LYMST
SHID_RAT
                                           5H1A_MOUSE
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STRAIN-Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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ID 545B RAT

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                                                                               August 31, 2004, 19:59:22 ; Search time 28.5 Seconds
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P60020
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P20905
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                        Compugen Ltd.
                                                           using frame_plus_n2p model
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compuo
                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
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5H5A_MOUSE
5H5A_RAT
5H1B_HUMAN
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SHIB_RABIT
SHII_DROME
SHID_CANFA
SHIB_CRIGR
SHIB_MOUSE
SHID_CAVPO
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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5H1B
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Match Length DB
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Database :

No.

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SO THE TETET

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ATCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCCATC 1024
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|ThralaargCysArgAlaThrValAlaPheGlnThrSerGlyAspSerTrpArgGluGln 291
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                                                          LeuCysCysThrAlaSerIleTrpAsnValAlaAlaIleAlaLeuAspArgTyrTrpThr
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|AlalleThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93196607; PubMed=8450829; M. dathes H., Boschert U., Amlaiky N., Grailhe R., Plassat J.-L., Matchelli F., Mattei M.-G., Hen R.; "Muscatelli F., Mattei M.-G., Hen R.; "Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors define a new family of serotonin receptors: cloning, functional expression, and chromosomal localization."; Mol. Pharmacol. 43:313-319(1993).
119 ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal---
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01-JUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine 5B receptor (5-HT-5B) (Serotonin receptor)
HTRSB OR SHTSB.
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CYTOPLARMIC (POTENTIAL).

CYTOPLARMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

8 SIMILARITY.
                                                                                                                                                    PIR; S38744; S38744.

InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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Conservative:
Mismatches:
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                                                                                               anxiety and depression.
SUBCELLULAR LOCATION: Integral membrane protein.
IISSUE SPECIFICITY: Expressed predominantly in the central nervous system; in the hippocampus, habenula, and the doral raphe.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
STRONGEST TO THE OTHER 5HT-5 SUBTYPE RECEPTORS.
FUNCTION: This is one of the several different receptors for 5-hydroxtryptamine (serotconin), a biogenia hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins. Probably involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGluValSerAsnLeuSerGlyAlaThrProGlyLeuAlaPheProProGlyProGlu
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
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MGD; MGI:96284; Htr5b.

InterPro; 1FR00016; GECR_Rhodpsn.

Prosolo1; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F2 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine 5A receptor (5-HT-5A) (Serotonin receptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM, 601305, -. Gintegral to plasma membrane, TAS. GO: GO:0005887, C:integral to plasma membrane, TAS. GO: 00005887, F:serotonin receptor activity, TAS. GO: 0007186; P:G-protein coupled receptor protein signalin. .., TAS. InterPro, IPR000276; GPCR_Rhodpsn.
                                                                                                                                                     TISSUE=Brain;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Puhl H.L. III, Ikeda S.R., Aronstam B.S.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: This is one of the several different receptors for 5-
In FUNCTION: This is one of the several different receptors for 5-
In Addroxytryptamine (serotomin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins.
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
STRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS.
                                                  MEDLINE=95080386; PubMed=7988681; Rees S., den Daas I., Foord S., Goodson S., Bull D., Kilpatrick G., Lee M.; "Cloning and characterisation of the human 5-HTSA serotonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00237; GFCRHODOPSN.
PROSTIE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSTIES; PS00263; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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Matches:
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CYTOPLASMIC (
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EMBL; X81412; CAA57168.1; JOINED.
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                                                                                                                   FEBS Lett. 355:242-246(1994)
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72.98%
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PIR; I37107; I37107.
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MIM; 601305; -.
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TGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCC 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 GAACTAGIGGCAGCGCIGGCCAIGCCACCGAGCCIGGCGAGIGAGCIGICGACCGGGCGA 364
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243 SerGluAlaValGluValLysAspSerAlaLys------GlnProGlnMetVal
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Mismatches:
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Matthes H., Boschert U., Amlainy N., Grailhe R., Plassat J.-L.,
Muscatelli F., Mattei M.-G., Hen R.,
"Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors
of define a new family of serotonin receptors: cloning, functional
expression, and chromosomal localization.";
Mol. Pharmacol. 43:313-319(1993).

I. FUNCTION: This is one of the several different receptors for 5-
hydroxytryptamine (serotonin), a biogenic hormone that functions
as a neurotransmitter, a hormone, and a mitogen. The activity of
this receptor is mediated by G protein.

I. SUBCELLULAR LOCATION: Integral membrane protein.

I. SUBCELLULAR LOCATION: Integral membrane protein.

I. TISSUE SPECIFICITY: Expressed predominantly in the central nervous
system; in the cerebral cortex, hippocampus, habenula, olfactory
bulb and granular layer of the cerebellum.

I. SIMCIARITY: Belongs to family 1 of G-protein coupled receptors.

STRONGEST TO THE OTHER 5HT-5 SUBTYPE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               TACACAGCTTTTAACAAGAACTACAATGCCTTCAAGAGCCTCTTTACTAAGCAG 1138
                              TyrThralaPheAsnLysAsnTyrAsnSerAlaPheLysAsnPhePheSerArgGln 356
                                                                                                                                                                                                                                                                                               MEDLINE-93099851; PubMed-1464308;
Plassat J.-L., Boschert U., Amlaiky N., Hen R.;
"The mouse 5HT5 receptor reveals a remarkable heterogeneity within
                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
5-hydroxytryptamine 5A receptor (5-HT-5A) (Serotomin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00237, GPCRRHODDSN.
PROSITE; PS0237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
Multigene family.

EXTRACRIATION (DATE: 140)

EXTRACRIATION (DATE: 140)
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                              357 AA.
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=93196607; PubMed=8450829;
                                                                                                                                                                                                                                                                                                                                       the 5HT1D receptor family.";
EMBO J. 11:4779-4786(1992).
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SEQUENCE FROM N.A.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
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                                                                   EXTRACELLULAR (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
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                 5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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	10 4 S		ALTERENTIALILY EXPRESSED IN TAI DEALN."; R. Proc. Natl. Acad. Sci. U.S.A. 90:3452-3456(1993). C! FUNCTION: This is one of the several different receptors for 5- C. hydroxytryptamine (serotonin), a biogenic hormone that functions C. as a neurotransmitter. a hormone, and a mitogen. The activity of this receptor is mediated by G proteins. C! SUBCELLULAR LOCATION: Integral membrane protein. C! SIMILARITY: Belongs to family 1 of G-protein coupled receptors. C: SIMILARITY: Belongs to family 1 of G-protein coupled receptors. C. C. STRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS. C. C. STRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS. C. C. STRONGEST TO THE OTHER SHT-6 SUBTYPE RECEPTORS.	the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and from this statement is not removed. Usage by and from send an email to license@isb-sib.ch). EMBL; 110072; AAA40515.1;

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                                                                                                                                                     857 AAAGCAACGGTGTCCTTCCAGGTGAGCGGGACTCCTGGCGGGAGCAGAAGGAGGGGGG
                                                                                                         MEDLINE=92246962; PubMed=1315531; Hamblin M.W., Metcalf M.A., McGuffin R.W., Karpells S.; Hamblin M.W., Metcalf M.A., McGuffin R.W., Karpells S.; "Molecular cloning and functional characterization of a human 5-HT1B serotonin receptor: a homologue of the rat 5-HT1B receptor with 5-HT1D-like pharmacological specificity."; Biochem. Biophys. Res. Commun. 184:752-759(1992).
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Kennedy J.L., Seeman P., van Tol H.H.M., Niznik H.B.;
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intronless gene on chromosome 6.";
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Biochem. Biophys. Res. Commun. 185:517-523(1992).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Human servionin ID receptor is encoded by a subfamily of two
"distinct genes: 5-HTID alpha and 5-HTID beta.";
Proc. Natl. Acad. Sci. U.S.A. 89:3630-3634(1992).
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01-DEC-1992 (Rel. 24, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
5-WAR-XXVXTYPEAMINE 1B receptor (5-HT-1B) (Seroto: (5-HT-1D-beta) (Serotoin 1D beta receptor) (S12)
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SEQUENCE FROM N.A.
MEDLINE-92218412; PubMed=1559993;
Levy F.O., Gudermann T., Perez-Reyes E., Birnbaumer M., Kaumann A.J.,
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SUBCELLULAR LOCATION: Integral membrane protein.
SUBCELLULAR LOCATION: Integral membrane protein.
PTM: Phosphorylated, and palmitoylated. Desensitization of the receptor may be mediated by its phosphorylation.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Strongest to the other 5HT-1 subtype receptors.
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Jin H., Oksenberg D., Ashkenazi A., Peroutka S.J., Duncan A.M.V.,
Rozmahel R., Yang Y., Mengod G., Palactios J.M., O'Dowd B.F.;
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"Molecular cloning of a human serotonin receptor (S12) with a pharmacological profile resembling that of the 5-HTID subtype."; J. Biol. Chem. 267:7553-7562(1992).
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"Cloning and plarmacological characterization of a novel human
"YdroxytryptaminelD receptor subtype.";
Mol. Pharmacol. 42:439-444(1992).
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Ng G.Y.K., George S.R., Zastawny R.L., Caron M., Bouvier M.,
Dennis M., O'Dowd B.F.;
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Biochem. Biophys. Res. Commun. 205:1194-1200(1994).
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"Silver project.";
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102 ValMetPro-----IleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGln 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGCGCTCATCGCCCCTCGCGCCGCTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGG 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG 814
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815 GAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC
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ID 5HIB PANTR STANDARD; PRT; 390 AA.

AC P60020;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)
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                                                                                                                                                                   GO: GO: 0005887; C:integral to plasma membrane; TAS.
GO: GO: 0004993; F:eerotonin receptor activity; TAS.
GO: GO: 0007187; F:eerotonin receptor activity; TAS.
GO: GO: 0007187; F:erotonin signaling, coupled to cyclic nucl. .; TAS.
GO: GO: 0007268; P:synaptic transmission; TAS.
InterPro: IRR000276; GPCR_Rhodpsn.
PFAm; PR00001; 7tm.1; 1.
PRNITS; PR00237; GPCRFHOOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
PROSITE; PS00262; G PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Bollymorphism anily; Lipoprotein; Palmitate; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 GGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTGCTAGTGCTGCTGATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 GCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 SerGlnAsnCysSerAlaLysAspTyrIleTyrGlnAspSerIleSerLeuPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-palmitoyl cysteine (Potential).
F -> C (in dbSNP:130060).
FTId=VAR 011715.
F -> L (in dbSNP:130061).
/FTId=VAR 011831.
/FTId=VAR 011831.
/FTId=VAR 011832.
E -> K (in dbSNP:130063).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 (POTENTIAL).
CYTOPLARMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CD874DC7EB44CF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Matches:
Conservative:
Mismatches:
Indels:
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    NOT ANNOTATED CDS
                                                       EMBL; AB041370; BAA94455.1; -.
EMBL; AY22527; AA067712.1; -.
EMBL; AL049595; CAB51837.1; -.
PIR; UNO268; UN0268.
Genew; HGNC: 5287; HTR1B.
MIM; 182131; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
M89478; -; NOT ANNOTATE
L09732; AAA36030.1; -.
M83180; AAA36029.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.31e-16
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48.35%
32.32%
20.80%
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TTCCTGACGGAACTCATCAGCCCACTCTGT-----GCCTGCAGCCTGCCCCCATCTGG 1027
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ArgSerArg11eLeuLysG1nThrProAsnArgThrG1yLysArgLeuThrArgAlaG1n 255
                               GGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTGCTAGTGCTGCTGCTGATCGCT 202
                                                                                                                                                                                                    ThrProAlaAsnTyrLeuIleAlaSerLeuAlaValThrAspLeuLeuValSerIleLeu 101
                                                                                                                                                                                                                                                                      102 ValMetPro-----IleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGln 119
                                                                                                                                                                                                                                                                                                       137 IleLeuHisLeuCysValileAlaLeuAspArgTyrTrpAlaIleThrAspAlaValGlu 156
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LysAlaThrLysThrLeuGlyIleIleLeuGlyAlaPheIleValCysTrpLeuProPhe 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
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                                                                                                                                                                                                                                      GCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGGGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCG
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 SerGlnAsnCysSerAlaLysAspTyrIleTyrGlnAspSerIleSerLeuPro----
                                                               -- TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu
                                                                                                   GCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCCACCATCCCGCGGGTCCGTGCCTTCCAC
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"Silver project."

Submitted (APR-200) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: This is one of the several different receptors for 5-
hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- FTM: Phosphorylated, and palmitoylated. Desensitization of the receptor may be mediated by its phosphorylation (By similarity).

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

Strongest to the other 5HT-1 subtype receptors.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
BY SIMILARITY.
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
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CD874DC7EB44CF12 CRC64;
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                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan
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                                              Pan troglodytes (Chimpanzee).
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                                                                                                                                        137 GGCCGAGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGCTGCTAGTGCTGCTG
                                                                                                                                                                                                                                                                      56 ThrLeuAlaThrThrLeuSerAsnAlaPheValIleAlaThrValTyrArgThrArgLys 75
                                                                                                            24 AsnLeuSerHisAsnCysSerAlaAspSerTyrIleTyrGlnAspSerIleAlaLeuPro
                           CCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGC---
                                                                                                                                                                  ----TrpLysvalLeuLeuvalAlaLeuLeuAlaLeuIle
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114 GlyGlnValValCysAspPheTrpLeuSerSerAsp
US-09-976-782-15 (1-1152) x 5H1B_SPAEH (1-386)
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                                                                                                                                                                                                                                      cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                         Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Spalacinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPIASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                         10-0CT-2003 (Rel. 36, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
HTR1B OR 5HT1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cysteine (Potential).
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1 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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7A006E021A44B7F4 CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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129
60
142
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Mismatches:
Indels:
                                          386 AA
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                                                                      15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43101 MW;
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32.66%
20.75%
                                          STANDARD;
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1109
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Best Local Similarity:
                                                                                                                                                                                                NCBI_TaxID=30637;
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                                          SPAEH
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DB:
                                                       P564<u>9</u>6;
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              RESULT 8
5H1B SPAEH
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556

919

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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                   6.49e-16
444.50
48.44%
32.55%
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198
387
                                  389 AA;
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31
121
387
                                                                                           Percent Similarity:
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                                                         Alignment Scores:
CARBOHYD
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            345 AlallePheAspPhePheAsnTrpLeuGlyTyrLeuAsnSerLeulleAsnProllelle 364
                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                           cyclase activity.
SUBCELIOLAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                           guinea
                                                                                                                                                                                                                       Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                     15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine lB receptor (5-HT-1B) (Serotonin receptor)
                                                                                                                                                                                                                                                                                                                   Zgombick J.M., Bard J.A., Kucharewicz S.A., Urquhart D.A., Weinshank R.L., Branchek T.A.; Wholecular cloning and pharmacological characterization of 6-HTLB and 5-HTLD receptors."; Neuropharmacology 36:513-524(1997).
                                                                         ||||||||
365 TyrThrMetProAsnGluAspPheLysGlnAlaPheHisLysLeu 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U82175; AABS8500.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PRIMT; PR000217; THI 1; 1.
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                         1082 TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL):
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MEDLINE=97368662; PubMed=9225276;
                                                                                                                               STANDARD;
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AlaAlaGlyMetileAlaLeuValTrpValPheSerIleCysIleSerLeuProPro-
                          S-palmitoyl cysteine (Potential).
CO57CABOA7FEE3C6 CRC64;
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Mismatches:
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Matches:
BY SIMILARITY
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Matches:
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                                                                         941 ATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTC 1000
                                                                                                                          -----GCCTGCAGCCTGCCCCCCATCTGGAAAGCATATTTCTGTGGCTTGGCTAC 1054
                                                                                                                                                                          1055 TCCAATTCTTCTTCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCC 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N [3]
SEQUENCE FROM N.A.
CSTRAIN=New Zealand white;
X MEDLINE=97032156; PubMed=8878052;
AB Bard J.A., Kucharewicz S.A., Zgombick J.M., Weinshank R.L.,
RA Bardchek T.A., Cohen M.L.;
RT "Differences in ligand binding profiles between cloned rabbit and human 5-HTID alpha and 5-HTID beta receptors: keranserin and human 5-HTID alpha and 5-HTID beta receptors: keranserin and RT methiothepin distinguish rabbit 5-HTID receptor subtypes.";
RL Naunyn Schmiedebergs Arch. Pharmacol. 354:237-244(1996).
CC -!- FUNCTION: This is one of the several different receptors for 5-C -- FUNCTION: This is one of the biogenic hormone that functions cC hydroxytryptamine (serotonin), a biogenic hormone that functions compared to the serotonin), a biogenic hormone that demylate
                                         -GAGAGGGAGCAGCCATGATGGTGGGAATTCTG 940
                                                                                                                                                 339 CysLysAspAlaCysTrpPheHisMetAlaIlePheAspPhePheThrTrpLeuGlyTyr 358
   ---AspAlaLeuLeu 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE-Saphenous vein;
Wurch T., Cathala C., Palmer C., Valentin J.P., John G.,
Colpaert F.C., Pauwels P.J.;
"Molecular cloning and identification of a rabbit saphenous vein 5-HT
IDB receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harwood G.S., Lockyer M., Giles H., Fairweather N.; "Cloning and characterisation of the rabbit 5-HTID alpha and 5-HTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBSECTION INTEGRATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                          ol-FEB-1996 (Rel. 33, Last Sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
mm.t. 1D-beta).
284 ValTyrValAsnGlnValLysValArgValSer--
                                                                                                                                                                                                                                                                                                  390 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96130324; PubMed=8543023;
                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta receptors.";
FEBS Lett. 377:73-76(1995).
                                                                                                                                                                                                                        1115 TTCAAGAGCCTC 1126
                                                                                                                                                                                                                                               379 PheHisLysLeu 382
                                                                                                                                                                                                                                                                                                STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
DIINNED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-palmitoyl cysteine (Potential).

G - S (IN RBF. 1 AND 3).

Q -> R (IN RBF. 1 AND 3).

MISSING (IN RBF. 1 AND 3).
                                                                                                                                                                                                       EMEL, X89731; CAA61883.1; -.

REBL; U60826; AAB58467.1; -.

PIR; S58126.

RICATE S68126.

InterPro; IPR000276; GPCR_Rhodpsn.

REAR, PR00001; 7tm 1; 1.

REAR, PR00001; 7tm 1; 1.

REAR, PR000101; 7tm 1; 1.

REOSITE; PS50227; GPRNHODDPSN.

REOSITE; PS50226; GPROTEIN RECEP F1 1; 1.

RECSITE; PS50226; GPROTEIN RECEP F1 2; 1.

G-Protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.

DOWAIN 1.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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C22EBC077C6C897D CRC64;
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CYTOPLASMIC (POTENTIAL).
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                                                                                     586
                                                                                                                                                                                                                 ---PhePheTrpArgGlnAlaLysAlaGluGluGluValSerGluCysLeuValAsnThr 203
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                             CTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGGCGCTGCCAGGTGAGCCGG 646
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CTGGGCCGCGACGGGCCATCACACGGCACCTGCAGCACACACGCTGCGCACCCGCAGCCGC
                                                                                                                             165 ArgAlaAlaIleMetIleArgLeuValTrpValPheSerIleCysIleSerLeuProPro 184
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STRAIN=Oregon.R; TISSUE=Head;
MEDLINE=91062395; PubMed=2174167;
Witz P., Amlaiky N., Plassat J.-L., Maroteaux L., Borrelli E., Hen R.;
"Cloning and characterization of a Drosophila serotonin receptor that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrThrSerValThrSerIleAsnSerArgAlaProAspValProSerGluSerGlySer
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                                                                                       GCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCGCCG
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15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine receptor 1 (5-HT receptor) (Serotonin receptor)
5-HT OR 5HT-R1 OR GG12073.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                 GTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTC-----
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
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Proc. Natl. Acad. Sci. U.S.A. 97:8940-8944(1990).

RE SEQUENCE FROW N.A.

SECURIOR FROW N.A.

SECURIOR FROW N.A.

SECURIOR FROW N.A.

SEQUENCE FROW N.A.

SECURIOR FROW N.A.

RESIDENCE OF C. Schere S.E. Li P.W. HOSEKIN B.A. Galle R.F.

A. Mannida P.G.: Schere S.E. Li P.W. HOSEKIN B.A. Mannida D. N. Hander P. Falandon N.C. Marked S.E. N. And D. N. Hand O. C. C. C. C. Schere S.G. C. Change P. Falandon N. Felfer B. D. M. Marked D. N. Mannida D. M. Marked D. N. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Mannida D. M. Man
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248 AlaSerileLeuAsnLeuCysAlaileSerValAspArgTyrLeuAlaileThrLysPro 2 497 CTGCAGCACACGCGCCCCGCGCCTGCTTGCTCATGATGCGCTCGCCGG 5 568 LeuGluTyrGlyValLysArgThrProArgArgMetMetLeuCysValGlyIleValTrp 2 557 GTGCGTCGGCGCTCATCGCCTCGCCGCTCTTTGGCCGGGCGAGGTGTGCGAC 6 558 LeuGluTyrGlyValLysArgThrProArgArgMetMetLeuCysValGlyIleValTrp 2 557 GTGCGTCGGCGCTCATCGCCTCGCCCTCTTTGGCCGGGGGAGGTGTGCGAC 6 558 LeuAlaAlaAlaCysIleSerLeuProProLeuLeuIleLeuGlyAsnGluHisGluAsp 3 617 GCTCGGCTCAGCGCTGCCAGGTGAGCCGGGAACCCTCTATGCCGCTTTCTCCACC 6 618 LeuAlaAlaAlaCysIleSerLeuProProLeuLeuIleLeuGlyAsnGluHisGluAsp 3 619 GTGGGCTCCAGCGCTTGGCGGGAACCCTCTATGCCGCTTTCTCCACC 6 619 GTGGGCCTTCCACCTGCCGCTTGGCGGGAACCTTCTCCACC 6 610 GTGGGCGCTTCCACCTGCCGCTTGGCGGGAACCTTCTCCACC 6 610 GTGGGCGCTTCCACCTGCCGCTTGGCGGTTGTTTTTTTTT	Db 361 ThrHisLeuGlnGlnAlaLeuAsnGlyThrGlySerPtcSerAlaProGlnAlaProPro 380 Qy 779 TTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGA	### STANDARD: #### STANDARD: #### STANDARD: #### STANDARD: #### STANDARD: ##### STANDARD: ##### STANDARD: ###### STANDARD: ########### ######################
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                                                                                                                                                                                                                                                              MEDLINE=92062181; PubMed=1659418;
Maenhaut C., van Sande J., Massart C., Dinsart C., Libert F.,
Monferini E., Givaldo E., Ladinsky H., Vassart G., Dumont J.E.;
"The orphan receptor cDNA RDC4 encodes a 5-HTID serotonin receptor.";
Biochem. Biophys. Res. Commun. 180:1460-1468(1991).
                                                                                                                                                                                                                                                                                                                                                                                                            "Expression and pharmacological characterization of a canine 5-hydroxytryptaminelD receptor subtype.";
Mol. Pharmacol. 40:1036-1042(1991)
-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                       ტ
                                        Libert F., Parmentier M., Lefort A., Dinsart C., van Sande J., Maenhaut C., Simons M.-2., Dumont J.E., Vassart G.; Salective amplification and cloning of four new members of the protein-coupled receptor family.";
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
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G protein coupled
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                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92100052; PubMed=1758439;
Zgombick J.M., Weinshank R.L., Macchi M., Schechter L.E.
Branchek T.A., Hartig P.R.;
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                              Dinsart C., va
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Libert F., Parmentier M., Lefort A., Dumont
"Complete nucleotide sequence of a putative
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PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0262; G PROTEIN RECEP F1 2; 1.
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
                           MEDLINE=89242119; PubMed=2541503;
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Multigene family.
DOMAIN 1
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|80 LysAlaGlnGluAspMetSerAspCysGlnValAsnThrSerGlnIleSerTyrThrIle
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Mismatches:
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---PhePheTrpArgGlnAlaLysAlaGluGluGluGluValLeuThrCysLeuValAsnThr
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200 AspHisValLeuTyrThrValTyrSerThrGlyGlyAlaPheTyrLeuProThrLeuLeu
                                                                                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                 S-palmitoyl cysteine (Potential).
BODC6211C2B6DECE CRC64;
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                          EXTRACELLULAR (POTENTIAL).
                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                MW;
                                                                                                                                                                                                                        1.1e-15
440.00
51.01%
34.78%
                                                                                                                                                                               42896
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 AA;
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Best Local Similarity:
 124 SerAsp
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                        DOMAIN
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                                                                                                                                      1009
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                                                                                                 --LeuPhePhe
                           GCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG---
                                                    275 AsnHisValGlnValLysLeuAla-----GludiyValLeuGluArgLysArglle
                                                                                 -----AAGGAGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTG
                                                                                                                                        DELCE ----
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ValCysTrpLeuProPhePheValAlaSerLeuValLeuProIleCysArgAlaSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                1070 AACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAG 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor).
                                                                                                                                      CTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; pr00001; 7tm 1; 1. PROSTER PROBLEM: pr00237; GPCRHODOPSN.
PROSTIE; PS00237; GPROTEIN RECEP F1 1; 1. PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1. G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
260 LeuGlnGluGluArgSerHisAlaAlaGlyProPro---
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (Chinese hamster)
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InterPro; IPR000276; GPCR Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                   STANDARD;
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109
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us-09-976-782-15.n2p.rsp

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                                                                                                                                                                                                                                 1051
                                                                                                                                                                                                                                                                                                           1012 TACTCCAATTCTTTCTAACCCCCTGATTTACACGCTTTTAACAAGAACTACAACAAT 1111
                                                                                                                                                                          ::::::||| |||::::::||||||:::|||||||:::
315 IleLeuGlyAlaPheIleValCysTrpLeuProPhePheIleIleSerLeuValMetPro 334
                                                                                                                                                                                                                                                                                                                               294
                                                                          937
                                                                                                                                                      997
                                                                                                                                                                                                                                                                     335 IleCysLysAspAlaCysTrpPheHisMetAlaThrLeuAspPhePheAsnTrpLeuGly 354
                                                                                                  GTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGG
                                    280 ProvalTyrValAsnGlnValLysValArgValSer------AspAlaLeu
                                                                                                                                                      CTGATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCA
                                                                                                                                                                                                                                 CTCTGT-----GCCTGCAGCCTGCCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGC
                                                                            GAGAGGCGAGCCATGATGGTGGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    localization in motor control centers.";

Proc. Natl. Acad. Sci. U.S.A. 89:3020-3024(1992).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse 5HT1B serotonin receptor: cloning, functional expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purkinje cells.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in striatum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maroteaux L., Saudou F., Amlaiky N., Boschert U., Plassat J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor).
HTRIB OR SHIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A.
MEDLINE=92212959; PubMed=1557407;
                                                                                                                                                                                                                                                                                                                                                                                       1112 GCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                            375 AlaPheHisLysLeu 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                          896 CGGGAGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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MGD; MGI:96274; Hrrlb.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7rm 1, 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

EMBL; Z11597; CAA77678.1; -. EMBL; M85151; AAA83221.1; -.

PIR; A42688; A42688

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CIGCCGGGC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 CGAGGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGCTGCTAGTGCTGCTGATC 199
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                                                                                                                                                                                                                                                                                                                                                                             38 GGCGTTGCCCTTGCCCTGGGACCCGAGACCAGCGGGACCCGGGACCCCAAGCCCGAGA 97
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| SlnValValCysAspPheTrpLeuSerAsp------IleThrCysCysThrAla
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TYOPIASNIAL).
N-LINKED (GLCMAC. . .) (POTENTIAL).
N-LINKED (GLCMAC. . .) (POTENTIAL).
                                                                                                                                                                                                                            S-palmitoyl cysteine (Potential), 58F70FBEA770C0B3 CRC64;
Transmembrane; Glycoprotein;
                                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                    EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                         CYTOPLASMIC (POTENTIAL)
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Mismatches:
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                                 (POTENTIAL)
                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                      7 (POTENTIAL)
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           Lipoprotein;
                                                                                                                                                                                                                                         43078 MW;
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438.00
48.22%
31.73%
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          family;
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437.50
45.98%
31.16%
20.31%
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PhePheIleIleSerLeuValMetProIleCysLysAspAlaCysTrpPheHisMetAla 345
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                  GluMetLeuAspCysPheValAsnThrAspHisValLeuTyrThrValTyrSerThrVal 210
                                                                                                                                                                                                                                   -----AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGlu 305
                                                                                                                                                                                                                                                                           ArgLysAlaThrLysThrLeuGlyIleIleLeuGlyAlaPheIleValCysTrpLeuPro 325
                                                                                                                                                                                                               -GAG
                                                      ---CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97368662; PubMed=9225276; Zgombick J.M., Bard J.A., Kucharewicz S.A., Urquhart D.A., Zgombick J.M., Branchek T.A.; Kucharewicz S.A., Urquhart D.A., Weinshank R.L., Branchek T.A.; Molecular cloning and pharmacological characterization of guinea pig 5-HT1B and 5-HT1D receptors."; Neuropharmacology 36:513-524(1997).

Neuropharmacology 36:513-524(1997).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions
CGGCTCCAGCGCTGCCAGGTGAGCCGGGAA---CCCTCCTATGCCGCCTTCTCCACCGG
                                          GGCGCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCG
                                                                                    -----GGCCGCCGC---CGGAGAGCT
                                                                                                       AlaArgSerArgIleLeuLysGlnThrProAsnLysThrGlyLysArgLeuThrArgAla
                                                                                                                                              GlnLeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgAla
                                                                                                                                                                    AAGGAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTG
                                                                                                                                                                                 ::: ||| ||| ::: ||| ProSerGluSerProValTyrValAsnGlnValLysValArgVal
                                                                                                                                                                                                                                                      AGGCGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGGATCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        060484; 008891; 0604891; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 5-hydroxytryptamine 1D receptor (5-HT-1D) (Serotonin receptor).
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STRAIN=Hartley, TISSUB=Brain;
STRAIN=97133356; PubMed=8978753;
Wurch T., Palmier C., Colpaert F.C., Pauwels P.J.;
"Sequence and functional analysis of cloned guinea parecronin S-HTID receptors: common pharmacological the 5-HTID receptor subfamily.";
J. Neurochem. 68:410-418(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity.

SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Strongest to the other 5HT-1 subtype receptors.
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CYTOPLEANTC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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R -> A (IN REF. 2).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS0262; GPROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family.
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EXTRACBLLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Non-endog Human 5-h

Human Human Amino aci Human ser

Serotonin Human 5-h

Amino aci

ser

Human Human

Non-endog

ser

Human Human

Murine 5H

Human

Rat REC17

Human LP3 Drosophil Fruit fly Dog 5-HT

Mouse isc Human ser

Serotonin

5-hydroxy

Human Human

HTR1A pro Human 5HT

Non-endog

Human

OM nucleic

Run on:

Sequence:

Searched:

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Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma; antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer; cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohn's disease; multiple sclerosis; Graft versus host disease;
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Aab47185 9
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ADC86157
AAU79252
ABP81980
AAE38595
ADES6996
                                                        AAR45848
AAU75167
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ABP81761
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2000US-0240637P.
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WO200230974-A2.
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Aae18654 Human G-p
Aam47211 Human NOV
Aae15638 Human G-p
Abg60235 Human G-p
Abg60235 Human hyd
Aar58686 Rat MR22
Ade56994 Rat Prote
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.

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The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like proteins; NOV3 is a collagen-like protein; NOV2a-d are keratin 1-like protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are cold inducible glycoprotein 30-like protein; NOV7 is a matrilin-2-like protein; NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic, and inducible glycoproteins with a management of antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and neuroprotective activities, and can be used in gene therapy. The NOVX sequences can be used in therapeutics, particularly for treating, preventing or alleviating and van be used in gene therapy. The NOVX sequences can be used in therapeutics, particularly for treating.

Creventing or alleviating an VOVX-associated disorder or a pathological state in a subject, particularly a disorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX collypeptide or nucleic acid, particularly cancer. The NOVX sequences are nucleic acid, particularly cancer. The NOVX sequences are especially useful in therapeutic or prophylactic applications for a disease associated with altered levels of sequences are nucleic acid, particularly cancer. The NOVX sequences are especially useful in therapeutic or prophylactic applications for a disease associated with the treatment of for particular and the treatment of the treatment of the presence of the presence of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the proce
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Ellerman K;
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                                                                                                                                                                                                                                                                                                       New NOVX polypeptides and polynucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
                                                                                                                                                                Spytek
                                                                                                                                         Mishra V;
                                                                                                                                         ook JP, Lepley DM, Burgess CE, Mishra V
Padigaru M, Shimkets RA, Zerhusen BD, S
n V, Macdougall J, Stone D, Gunther E,
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                                                                  CURAGEN CORP.
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N-PSDB; ABN86917.
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Edinger S,
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81 ArgvalArgAlaPheHisArgvalProHisAsnLeuValAlaSerThrAlaValSerAsp
                                                      GluLeuValAlaAlaLeuAlaMetProProSerLeuAlaSerGluLeuSerThrGlyArg
                                                                                           CGTCGGCTGCTGGGCCCGGAGCCTGTGCCACGTGGATCTCCTTCGACGCCGGAGCCTGT
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                                     GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA
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 TICTCCACCCGCGGCGCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAG
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The present invention provides the protein and coding sequences pf novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV3, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, NOV9, N
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                                                                                                                                                                                                                                                                                                                                                                                                                 New G protein-coupled receptor related polypeptides and polynucleotides for diagnosis, prevention and treatment of metabolic, neurodegenerative, retinal, immune, hematopoietic disorders, diabetes, obesity and
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Liu X, Patturajan M, Gusev VY;
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Indels:
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06-APR-2000; 2000US-019508BP.
10-APR-2000; 2000US-019592P.
11-APR-2000; 2000US-019655BP.
13-APR-2000; 2000US-0197081P.
14-APR-2000; 2000US-0197087P.
14-APR-2001; 2000US-0197525P.
29-MAR-2001; 2001US-00823187.
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97.36%
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Spytek KA,
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Best Local Similarity:
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Isolated human G-protein coupled receptor polypeptides and the use of these sequences in the diagnosis, treatment and prevention of diseases and in the assessment of exogenous compounds on the expression of the
                                                                                                                                                                                                                       Hafalia AJA, Nguyen DB, Gandhi AR,
Khan FA, Patterson C, Lu DAM, Tx
Farul R, Yeo MG, Yang J, Ramkumar J
idez R, Walsh RT, Borowsky ML, Thor
'label= Mature_GCREC_8_protein
          300. .318
/label= Transmembrane domain
                                                                                                           16-JUN-2000; 2000US-0212483P.
22-JUN-2000; 2000US-0213954P.
29-JUN-2000; 2000US-0215209P.
07-JUL-2000; 2000US-0218555P.
14-JUL-2000; 2000US-0218936P.
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21-JUL-2000; 2000US-0220141P.
                                                                                       15-JUN-2001; 2001WO-US019275
                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
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Griffin JA, Yue ..
.. Y, Walia NK, Grau. ..
... Y. Hernandez R, P
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cal Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 372 AA;
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                                            WO200198351-A2
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  484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>AAGGAGAGGGGGGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGTGCTGG</u>
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                                                          ATCTACGAGGCGGCCAAGTTTCGGCTGCCGCCGCCGGAGAGCTGTGCCG
                                                                                                                                                                                                                                                                                           256 AlaThrMetGln------ValLysGluAlaProAspGluAlaGluValValPhe
               PheSerThrArgGlyAlaPheHisLeuProLeuGlyValAlaProPheValTyrArgLys
                                                                                                                                                                                                                                                                       GCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTC
                                                                                         GCGCTCGCCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCGCCGCTGCTCTTTGGCCGGGGC
                                                                                                                                    GAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC
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/label= Signal_peptide
48..6 Transmembrane_domain
66..372
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Ramkumar J, Au-You / ML, Thornton M,

Kallick DA; Au-Young Jon M, He ? Tribouley CM;

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The invention relates to isolated human G-protein coupled receptor (GCREC) polypeptides and their biologically active fragments. GCREC and protein is useful in treating a disease or condition associated with an increase or decrease in expression of functional GCREC. The GCREC's are useful in the diagnosis, treatment and prevention of cell proliferative disorders (cancer, leukaemia, melanoma); neurological disorders (stroke, epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris); gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis), metabolic disorders (diabetes); viral inflections (herpes virus) and in the assessment of the effects of exogenous compounds on the expression of the nucleic acid and amino acid sequences. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 GCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTCTTCACGGTCCTGGTGACGCTG 184
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Claim 1; Page 121; 143pp; English.
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vascular disorder; infectious disease; anorexia; cancer; stroke; neurodegenerative disorder, Alzheimer's disease; acute brain injury; central nervous system disorder; depression; lung disorder; eproductive disorder; tissue disorder; thrombocytopaenia; migraine; angiogenesis; asthma; X-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disorder; hepatitis; fertility; hypertension; arteriosclerosis; ischaemia; rheumatoid arthritis; Grave's disease; wound healing.
                      Human; NOVX; developmental disorder; endocrine disorder;
Human hydroxytryptamine receptor-like protein NOV8.
                                                                                                                                                                                                                           15-SEP-2000; 2000US-0232675P.
15-SEP-2000; 2000US-0232676P.
16-SEP-2000; 2000US-023362P.
18-SEP-2000; 2000US-0233402P.
19-SEP-2000; 2000US-0233521P.
19-SEP-2000; 2000US-0233521P.
19-SEP-2000; 2000US-0233522P.
19-SEP-2000; 2000US-023360P.
20-SEP-2000; 2000US-0233899P.
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2000US-0240498P.
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2001US-0264274P.
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                                                                                                                                          Homo sapiens.
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13-OCT-2000;
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Colman SD; Tchernev VT; G, Millet I; Syptek KA, Taupier RJ, Vernet CAM, thernev VT, Malyankar UM, Shency S, Patturajan M, Burgess CE, Smithson stone D, Gunther E, Ellerman K; Syptek KA, Tchernev VT, Stone D, Padigaru M, Mishra VS, Gorman L, Peyman JA,

2001US-0274862P

09-MAR-2001;

(CURA-) CURAGEN CORP

WPI; 2002-383182/41. N-PSDB; ABK71923 New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumors, lung disorders, hematopoletic disorders, autoimmune diseases and immune disorders.

Claim 1 ; Page 60; 210pp; English.

The invention relates to an isolated NOVX polypeptide selected from NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1b, NOV1a, NOV1b, NOV1a, NOV1b, NOV1a, NOV1b, Nov1b, Nov1

ABG60235 standard; protein; 380 AA.

30-JUL-2002 (first entry)

ABG60235;

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1045

925 308 985

CCTGACGGAA

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CTTGGCTACTCCAATTCTTTCTTCAACCCCCTGATTTACACAGGCTTTTAACAAGAACTAC 1105
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sensory; motor; behaviour; central nervous system; CNS; superfamily; G-protein; ligand-gated; ion channel; subfamily; human; rat; amplify; primer; PCR; amplification; brain; hypothalamus; indolamine; drug; hypothalamus; therapeutic; neurological; pathology; dementia; insomni
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 migraines, inflammation, autoimmune disorders, disorders affecting sleep, appetite, thermoregulation, pain, perception, hormone secretion and sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, tramma, regeneration, viral, bacterial or parasitic infections, hyper- or hypo-thyroidism, endometriosis, fertility, hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked mental retardation, psychotic and neurological disorders and neuronal degeneration. The present sequence represents a NOVX protein
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comprising the vector compressed in an animal subjected to pain and a subjected to pain, a method for identifying a compound which regulates the expression of the polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the activity in an animal of one or more of the composition, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound useful that regulates the activity in an animal of one or more of the polypeptides given in the contract of the polymentides of the contract of the natural of one or more of the polypeptides given in the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the contract of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the contract of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of the polymentides of 
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01-NOV-2001; 2001US-0346382P.
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        ATGGAGGCCCCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACCCGAG
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                        79 ArgValArgAlaPheHisArgValProHisAsnLeuValAlaSerThrAlaValSerAsp
                                                                                                                                                                                             216 PheSerThrCysGlyAlaPheTyrLeuProLeuAlaValValLeuPheValTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 ThrAlaArgArgArgAlaThrValThrPheGlnThrSerGlyAspSerTrpArgGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 LysGluLysArgAlaAlaMetMetValGlyIleLeuIleGlyValPheValLeuCysTrp
                                                                                                                                                                                                                                                                                                                                        CTGTGCTGCCCCCCCCCGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCCGCGACGGGGCC
                                                                                                                                                                                                                                                                                                                                                                             136 LeuCysCysThrAlaSerIleTrpAsnValAlaAlaIleAlaLeuAspArgTyrTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTCCACCGCGCGCCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725 ATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCCGGAGAGCTGTGCTGCCGTTGCCG
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                                                                                   CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACACGCCACCTGCACACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to transgenic animals, compositions and methods relating to the characterisation of gene function. The invention also relates to transgenic mice comprising mutations in 5-hydroxy-tryptophan (5-HT)5B receptor gene. The transgenic mice are useful for identifying an agent that modulates the phenotype such as increased depression or increased pain sensitivity. They are also useful for identifying potential therapeutic agents for the treatment of pain or depression and for evaluating a potential therapeutic agent capable of affecting a condition associated with a mutation in a 5-HT5B receptor gene. Transgenic animals of the invention are also useful for testing the efficacy of proposed genetic and pharmacological therapies for human diseases such as neurological, neuropsychological or psychotic illnesses. The present sequence is mouse 5-HT5B receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGCTG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGluValSerAsnLeuSerGlyAlaThrProGlyLeuAlaPheProProGlyProGlu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel transgenic mouse useful for identifying a potential therapeutic agent for the treatment of depression or pain, comprises disruption in 5-hydroxytryptophan 5B receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGAGGCCGCTATCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACCCGAG
                                                                                                 Mouse; 5-hydroxytryptophan; 5-HT5B receptor; depression; transgenic; transgenic animal; phenotype; pain sensitivity; neurological disease; gene therapy; pharmacological; neuropsychological disease; analgesic; psychotic illness; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ACCAGCAGCGGACCCCGAGCCCCAAGCCCGAGAGATACTCGGTTCGACCCCCGAGCGGC
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298
119
53
3
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Conservative:
Mismatches:
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                                                                  receptor protein.
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1452.50
83.64%
78.63%
67.43%
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21-DEC-2001; 2001US-0342472P.
28-MAR-2002; 2002US-00109532.
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                   (first entry)
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N-PSDB; AAD48747.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 370 AA;
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                                                             5-HT5B
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                   07-MAR-2003
                                                                                                                                                                                                                                                                                              10-OCT-2002
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Pred. No.:
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433 601 453 661 473 721 493 781

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CGACGICGGCIGCIGGGCCGGAGCCIGIGCCACGIGIGGAICTCCTICGACGCCGGAGCC 421
                    394 ArgLeuCysCysProAlaGlyLeuGlyAsnValAlaAlaIleAlaLeuGlyArgAspGly
                                                                                                                                                   414 AlalleThrArgHisLeuGlnHisThrLeuArgThrArgSerArgAlaSerLeuLeuMet
                                                                                                                                                                                                                   434 IleAlaLeuAlaArgValProSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyArg
                                                                                                                                                                                                                                                                                    GlyGluValCysAspAlaArgLeuGlnArgCysGlnValSerArgGluProSerTyrAla
                                                                                                                                                                                                                                                                                                                                                     474 AlaPheSerThrArgGlyAlaPheHisLeuProLeuGlyValValProPheValTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                 422 TGTCTGTGCCCCGCCCGCCGCCGCCTCGGGAACGTGGCCGCCATCGCCCTGGGCCGCGACGGG
                                                                                                                                GCCATCACACGCACCTGCAGCACACGCTGCGCACCCGCAGCCGCGCGCCTCGTTGCTCATG
                                                                                                                                                                                                  ATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCGCCGCTGCTCTTTGGCCGG
                                                                                                                                                                                                                                                                 GGCGAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCC
                                                                                                                                                                                                                                                                                                                                 GCCTTCTCCACCCGCGCGCCTTCCACCTGCCGCTTGGCGTGCCGGTTTGTCTACCGG
                                                                                                                                                                                                                                                                                                                                                                                                  722 AAGATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCCGCGGAGAGCTGTGCTGCCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TCCAGGTGAGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective; neurological disease; depression; epilepsy; gene therapy; single nucleotide polymorphism; haplotype pair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GGGAGCAGAAGGAGGC 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5-hydroxytryptamine receptor 5A; HTR5A; serotonin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGCCACCATGCAGGTGAGGTCCAAGGTA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2000; 2000US-0233051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triphosphate-binding protein coupled receptor (GPCR). A polymucleotide of the invention may have a use in gene therapy. The polymucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyAlaValLeuProGlyArgGlyProProPheSerValPheThrValLeuValValThr 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgProAlaAlaGlyProGlyThrProSerProArgGlyIleLeuGlySerThrProSer 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACCAGCAGC-GGACCCCGAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGCCGTCCTGCCGGGCCGAGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACG 181
                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACCCG
                              GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a novel polynucleotide encoding a guanosine
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274
6
33
5
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 610; 28pp; English
ID NO:610
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                                                                                                                                                                                                                                                                                              Asai K, Akiyama Y,
                                                                                                                                                                             18-JUN-2002; 2002EP-00013517
                                                                                                                                                                                                               18-JUN-2001; 2001JP-00246789
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1296.50
83.33*
81.55*
Human GPCR protein SEQ
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N-PSDB; ADC86156.
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                                                                                Homo sapiens
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PheThrValArg---HisAlaThrValThrPheGlnProGluGlyAspThrTrpArgGlu 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLysGluGlnArgAlaAlaLeuMetValGlyIleLeuIleGlyValPheValLeuCys 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1082 TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAG 1138
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                                                                                                                                                   TTCTCCACCCCCGCGCCCTTCCACCTGCCCCTTGGCGTGCCCGTTTGTCTACCGGAAG
                                                                                                                                                                           203 PheSerThrValGlyAlaPheTyrLeuProLeuCysValValLeuPheValTyrTrpLys
                                                                                                                                                                                                                                     ATCTACGAGGCGGCCAAGTTTCGTTTCGGC----CGCCGCCGGAGAGCTGTGCTGCCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAAGGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGT
                                                              GAGGIGIGOGACGCICCGGCICCAGCGCIGCCAGGIGAGCCGGGAACCCICCIAIGCCGCC
                                                                                                                                                                                                                                                                                                                   782 CCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTG
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                                                                                                                                                                  The invention relates to single nucleotide polymorphisms in the gene encoding human 5-hydroxytryptamine (serotonin) receptor SA (HTR5A). A method for haplotyping the HTR5A gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and etermining whether one of the copies of the gene is defined by one of the HTR5A haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a triait and a haplotype or haplotype or pair of the HTR5A gene can be identified by comparing the frequency of the haplotype or haplotype frequency of the haplotype or haplotype frequency in the trait population. The frequency of the haplotype of haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype or haplotype or haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype or haplotype or haplotype frequency of tunction of HTR5A, and in screening for candidate drugs to treat diseases related to HTRSA activity, such as neurological disorders, including configuration and epilepsy. This sequence represents the human HTRSA
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|ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp
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| LeuGlyPheLeuValAlaAlaThrPheAlaTrpAsnLeuLeuValLeuAlaThrIleLeu
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                                                    5A
                                                 Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor isogenes, useful for improving efficiency and reliability in drug development for treating neurological diseases.
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Mismatches:
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                                                                                                                                      Claim 31; Fig 4; 134pp; English.
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1063.50
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             N-PSDB; ABK50434.
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The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular Gretien-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or aridity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzhaimer's disease, atherosclerosis, bacterial, fungal, protoscan or viral infections.
                                                                                                      New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host lisease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypetrension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42669 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ACCAGCAGCGGACCCGGGACCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGGAGCGGC 124
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Brown JP;
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1063.50
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Roush CL,
                                                                                                                                                                         autoimmune diseases.
                                         WPI; 2003-046718/04.
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                                                              N-PSDB; ABZ42828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, urological disorder; urinary incontinence; gene therapy, cancer; kidney disorder, overactive, oversensitive bladder; dysfunction; bladder; urethra, overflow urinary incontinence; stress urinary incontinence; nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;
                                                                                                         604
                                                                                                                                                                                                                                                                                                   223 ileTyrLysAlaAlaLysPheArgValGlySerArgLysThrAsnSerValSerProIle 242
                                                                                                                                                                                                                                                                                                                                                 CTGTGCTGCCCCCCCGGCCTCGGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGGGCC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLysGluGlnArgAlaAlaLeuMetValGly1leLeuIleGlyValPheValLeuCys 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 TyrThralaPheAsnLysAsnTyrAsnSeralaPheLysAsnPhePheSerArgGln 356
                      LeuCysCysThrAlaSerIleTrpAsnValThrAlaIleAlaLeuAspArgTyrTrpSer
                                                                                                                                                                                 203 PheSerThrValGlyAlaPheTyrLeuProLeuCysValValLeuPheValTyrTrpLys
                                                                    CCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTG
                                                    ATCACACGGCACCTGCACACGCTGCGCACCCGCAGCCGCCTCGTTGCTCATGATC
                                                                                                         AlaLeuThrTrpAlaLeuSerAlaValIleSerLeuAlaProLeuLeuPheGlyTrpGly
                                                                                                                                                                GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC
                                                                                                                                                                                                                     TTCTCCACCGCGCGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG
                                                                                                                                                                                                                                                                           ATCTACGAGGGGGCCCAAGTTTCGTTTCGGC----CGCCGCCGGAGAGCTGTGCTGCCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 5-hydroxytryptamine 5A (5-HT-5A) (serotonin receptor), 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38595 standard; protein; 357 AA
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365 CGTCGGCTGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424

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                                                                                                                                                                                                                                                                                CAGAAGGAGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGC
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                     GAGGTGTGCGACGCTCGGGTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC
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183 GluThrTyrSerGluGlySerGluGluCysGlnValSerArgGluProSerTyrAlaVal
                                                                                                                                                                                                                                                               AICTACGAGGCGGCCAAGITICGITITCGGC---CGCCGCCGGAGAGCIGTGCTGCCGTTG
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   ATCACACGGCACCTGCACACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC
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                                                                   GCGCTCGCCCGGGTGCCGTCGCCGCTCATCGCCCTCGCCGCCGCTGCTCTTTGGCCGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Protein NP 076917, SEQ ID NO 2851.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                The present relates to a method for identifying a compound for treating uvological disorders e.g., urinary incontinence including overactive/ oversensitive bladder, overflow urinary incontinence, stress urinary incontinence caused by dysfunction of the bladder, urethra or central or peripheral nervous system, prostatitis, benign prostatic hyperplasia, cancer of the prostate or kidney disorders. The method is also useful for urological disorder. The invention is also used in gene therapy. The present sequence is human GPCR known as 5-hydroxytryptamine 5A (5-HT-5A) (serotonin receptor)
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                                                                                                                                                                                                                                                             Identifying a compound for treating urological disorders, for example urinary incontinence by assaying the ability of the compound to modulate the nucleic acid expression or polypeptide activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGCTTCCGGTCACCATCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGTGCTGCCCCGCCGGCCTCGGGAACGTGGCCGATCGCCCTGGGGCCGCGACGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ThrserPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCGGCTGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 ArgvalArgThrPheHisArgvalProHisAsnLeuValAlaSerMetAlaValSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                Karicheti V;
28-FEB-2002; 2002US-0360500P.
15-MR-2002; 2002US-0355041P.
19-ARR-2002; 2002US-0374053P.
14-AUG-2002; 2002US-0403468P.
27-SEP-2002; 2002US-0419368P.
05-NOV-2002; 2002US-0419366P.
                                                                                                                26-NOV-2002; 2002US-0429797P
                                                                                                                                                MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.73e-74
1063.50
72.98%
62.95%
49.37%
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                                                                                                                                                                                Silos-Santiago I,
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urinary inco
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106 ArgTrpGlnLeuGlyArgArgLeuCysGlnLeuTrpIleAlaCysAspVal----- 122

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Costigan M;
 Befort K,
D'urso D,
                      WPI; 2003-268312/26
                                  GENBANK; NP 076917
ΰ
Woolf
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English

The inversion discusses a composition which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a which is differentially regulated in an animal subjected to pain an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence which is differentially expressed in neuronal tissue of a first animal composition of a polynuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially expressed in an animal subjected to pain, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more composition activity in an animal of one or more of the polynectides given in the compound a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more conjugates its activity is useful for preparing a medicament for treating pain and e.g. spinal segmental nerve injury (CNI) in an animal (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. spinal segmental reversed discendent (e.g. spinal part). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed print/pub/published_pot_sequence of the properticent of the composition of the print of the print of the propertice invention discloses a composition comprising two or more isolated

Sequence 357 AA;

357 226 36 86 11 Matches: Conservative: Mismatches: Indels: 2.73e-74 1063.50 72.98% 62.95% 49.37% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

US-09-976-782-15 (1-1152) x ADE56996 (1-357)

ACCAGCAGCGGACCCGGGACCCCAAGCCCGAGGGGATACTCGGTTCGACCCCGAGCGGC 124 GCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGCTG ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp æ a 셤 à 8

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GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA 364

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CGTCGGCTGCTGGGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424 365

AICIGGAAAAGCATAITICIGTGGCTTGGCTACTCCAATTCTTTCTACCCCCCTGATT 1081 484 162 TGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCC 1021 ||||||||| |LeuCysCysThrAlaSerIleTrpAsnValThrAlaIleAlaLeuAspArgTyrTrpSer 142 604 664 724 781 242 841 901 277 961 TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAG 1138 |||| |GluThrTyrSerGluGlySerGluGluCysGlnValSerArgGluProSerTyrAlaVal 318 ileTrpLysSerIlePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle CTGTGCTGCCCCGCCGGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGGGCC GCGCTCGCCCGGGCCGTCGGCGCTCATCGCCCTCGCGCCGCTGCTTTTGGCCGGGGC GAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTATGCCGCC SerGluAlaValGluValLysAspSerAlaLys------GlnProGlnMetVal TTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAG CAGAAGGAGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGC TTCTCCACCGCGCGCCCTTCCACCTGCCGCTTGGCGTGCTGCTGTTTGTCTACCGGAAG ATCTACGAGGCGGCCAAGTTTCGTTTCGGC----CGCCGGCGGAGAGCTGTGCCTGCCGTTG CCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTG 298 123 485 143 545 183 782 243 278 1082 425 605 999 203 725 223 842 902 962 1022 338 à g à g ð a δ Пр à g ð qq à g ò q ð 셤 à 셤 à g à

Search completed: August 31, 2004, 20:15:04 Job time : 175.5 secs

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OBSP12 caenorhabdi Ognor
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09n2d9 pan troglod
09n2d7 pongo pygma
09n2b6 pan troglod
09n2b6 gorilla gor
197842 rattus norv
09n2b4 pongo pygma
09g4i2 sus scrofa
09g4i2 haemonchus
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Q8jg69 brachydanio
Q90wy4 brachydanio
Q7t1a2 brachydanio
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Q9gk99 canis famil
Q9my18 oryctolagus
Q8cg15 mus musculu
Q9db10 mus musculu
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Q98998 xenopus lae
Q9n263 sus scrofa
Q8sph2 sus scrofa
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Q9glp5 sus scrofa
Q8buw7 mus musculu
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Q9ng02 apis mellif
O77254 boophilus m
 986unl homo sapien
9n2b7 gorilla gor
Q99mb0 mesocricetu
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O44198 apis mellif
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                                       Q8hyb0 canis famil
                                                    099q54 aedes aegyp
076267 aplysia cal
09n297 gorilla gor
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8awel brac
Q925k7 mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 24, Last sequence update)
S1:2C12P8.3 (Novel protein similar to human 5-hydroxytryptamine (Serotonin) receptor 5A (HTR5A)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corby N.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL772146; CAD61100.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IERN00276; GPCR_Rhodopsin.
PF00001; 7tm_1; 1.
                                                                                                                                                                                                                Q8sph2
Q8mx83
Q9n2d8
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Q9N263
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P97842
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Q8JG03
Q9NG02
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Q9BMA9
Q8JG69
                         Q99MB0
Q8HYB0
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Q8BZP1
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Q9GLP5
Q8BUW7
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Q8CGI5
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Q925K7
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Q9N297
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Q8MX83
Q9N2D8
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Q9N2D9
Q9N2D7
Q9N2B6
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Q9GK99
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 SEQUENCE FROM N.A.
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                          Compugen Ltd.
                                                                OM nucleic - protein search, using frame_plus_n2p model
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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                                                                                                                 319 AsnSerPhePheAsnProLeulleTyrThrAlaPheAsnLysAsnTyrAsnAsnAlaPhe
279 LeulleGlyValPheValLeuCysTrpIleProPhePheLeuAlaGluLeuIleIlePro
                                                   AATTCTTTCTTCTACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTC
                                  CTCTGTGCCTGCCCTGCCCCCCCTTGGAAAAGCATATTTCTGTGGCTTGGCTACTCC
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

B MBL; AC093726; AAP21864.1; ---

R GO: GO:0015602; C:integral to membrane; IEA.

GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO: GO:000186; P:canscription factor activity; IEA.

GO: GO:0007186; P:canscription factor activity; IEA.

GO: GO:0007186; P:canscription of transcription, DNA-dependent; IEA.

R GO: GO:0007186; P:canscription of transcription, DNA-dependent; IEA.

R GO: GO:0007187; FRXENDOPSN.

R PROSTIE; PS00001; Ttml LysR.

R PROSTIE; PS000237; GPCRHODOPSN.

R PROSTIE; PS00044; HTH_LYSR_FAMILY; 1.

R PROSTIE; PS00044; HTH_LYSR_FAMILY; 1.

R HYDOLHETICAL protein.

HYDOLHETICAL POCCEN.

R HYDOLHETICAL PROTEIN.

SEQÜENCE 247 AA; 27470 MW; 38771F8BBF0137B6 CRC64;
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Catarrhini, Hominidae, Homo.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein HTR5A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ
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                                                                                                                                                                                    339 ArgAsnLeuPheSerArgGlnArg 346
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                   1118 AAGAGCCTCTTTACTAAGCAGAGA
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Suleton J.B., Waterston R.;
"Toward a complete human genome se
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE FROM N.A.
Waterston R.;
Submitted (MAR-2002) t
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Submitted (FEB-2002)
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Submitted (FEB-2002)
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Pred. No.:
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|IleSerCysAspVal-----LeuCysCysThrAlaSerIleTrpAsnValThrAla
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LysThrAsnThrIleThrProMetAlaGluValIleGlu-------ValLysGlu
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|AlaGluArgGlnProGlnMetAlaPheThrValArg---HisAlaThrValSerPheGln
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                                                                                                                                                                                                                                                   101 ATACTCGGTTCGACCCCGAGCGGCGCCGTCCTGCCGGGCCGAGGGCCGCCCTTCTCTGTC
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 PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECRE F1 1; 1.
PROSITE; PS50262; G PROTEIN RECRE F1 2; 1.
SEQUENCE 346 AA; 39412 MW; BS54DIBC1E74413E CRC64;
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216
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73
73
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Mismatches:
Indels:
Gaps:
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||leSerGlyGlySerGluSerGlyAsnLeuTyr
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                                                                                              3.99e-62
1050.50
74.71%
62.07%
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Best Local Similarity:
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CCCGAGACCAGCAGCGGGACCCGGGACCCCAAGCCCGGAGAGGGATACTCGGTTCGACCCCG 118
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|10 ProPro***ProAlaGlySerGluThrTrpValProGlnAlaAsnLeuSerSerAlaPro
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                                                                            37D54B95E3277FC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     PERNYS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 390 AA; 43565 MW; 37D54B95E3277FC3 CRC6
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Matches:
Conservative:
Mismatches:
Indels:
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451.00
48.35%
32.32%
20.94%
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                                  SEQUENCE FROM N.A. STRAIN=gorilla-U1;
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|LeuCysCysThrAlaSerIleTrpAsnValThrAlaIleAlaLeuAspArgTyrTrpSer 142
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163 AlaLeuThrTrpAlaLeuSerAlaVall1eSerLeuAlaProLeuLeuPheGlyTrpGly 182
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Sukaryota, Metazoa, Chordata; Craniata, Vertebrata; Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae, Gorilla.
NCBI_TaxID=9593;
  143
22
74
6
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                         Conservative:
Mismatches:
Indels:
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01-0CT-2000 (TEMBLRel. 15, Last seq
01-JUN-2003 (TEMBLRel. 24, Last ann
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AspvalProSerGluSerGlySerProValTyrValAsnGlnValLysValArgValSer
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1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL. AR25654, AAXESB27.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; P:d-protein coupled receptor protein signalin. .;

PEAM: PP000021; Ttm_1: 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Devor E.J., Devor R.M.;
"Cloning and sequencing the serotonin receptor SHTIB in the Hamster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANKIS, PRO0237; GPCKRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS002025; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 386 AA, 43020 MW; 19F430C36F5CEB40 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Serotonin receptor 5HT1B.
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|SerLeuAlaValThrAspLeuLeuValSerIleLeuValMetProValSerThrMetTyr
                                                                                                                                                                                                                                                                                                                                                                              GAGCTGTCGACCGGGCGACGTCGGCTGCTGGCCGGAGCCTGTGCCACGTGTGGATCTCC
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124 SerAsp-----IleThrCysCysThrAlaSerIleMetHisLeuCysVallleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 LeuAspArgTyrTrpAlaIleThrAspAlaValGluTyrSerAlaLysArgThrProLys
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                                                                                                                                                                                                                                                              407 INCGACGCCGGAGCCTGTCTGTGCTGCCCCGCCGGCGCAACGTGGCGGCGCCATCGCC
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|ProValTyrValAsnGlnValLysValArgValSer-----
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                                    Conservative:
Mismatches:
                    Matches:
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3.29e-21
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980 ACGGAACTCATCAGCCCACTCTGT-----GCCTGCAGCCTGCCCCCCATCTGGAAAAGC 1033
                                                      AspLeuPheileAlaLeuAspVal------LeuCysCysThrSerSerIleLeuHis 126
                     CACGTGTGGATCTCCTTCGACGCCGGAGCCTGTCTGTGCTGCCCCGCCGGCGTCGGGGAAC 451
                                                                                                                                                                                                                                             ATCGCCCTCGCGCCGCTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGCGC 631
                                                                                                                                                                                                                                                                            167 ileSerileProProMetLeuGlyTrpArgThrProGluAspArgSerAspProAspAla 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 ArgGlnGlyProGlySerLysAlaGlyGlyProLeuCysThrAsnGlyAlaValArgArg 283
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                                                                                                                                                                                           :::
LysArgThrProArgArgAlaAlaAlaLeuIleSerLeuThrTrpLeuIleGlyPheLeu
                                                                                            GTGGCGGCCATCGCCCTGGGCCGCGACGGGCCATCACACGGCACCTGCAGCACACGCTG
                                                                                                                                                                  CGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCCGGGTGCCGTCGGCGCTC
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|YsthrileSerLysAspHisGlyTyrThrileTyrSerThrPheGlyAlaPheTyrile
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1052 TACTCCAATTCTTTCTTCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAAGAT 1111
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                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                           van den Berg L., Versteeg S., van Oost B.; "Isolation and characterization of the canine serotonin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene (HTRIA).";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AT134445; AAN08044.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro: IPRO00276; GPCR_Rhodopsn.
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3 GlyLeuSerProArgGlnGlyAsnAsnThrThrSerSerGluGly----
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Last annotation update)
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Matches:
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Gaps:
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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                                                                       GCCTTCAAGAGCCTC 1126
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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359 IleMetSerAlaPheThrValCysTrpLeuProPhePheIleLeuAlaLeuValArgPro 378
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                                                                                                                                                                                                                                          MetLeuphevalTyrpheGlnIlePheArgAlaAlaArgArgIleValAsnGluGluLys 305
                                                                                                                                                                                                                                                                                AGAGCIGIGCIGCCGIIGCCGGCCACCAIGCAGGIGAGGICCAAGGIAAAGGAAGCACCI 823
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Apogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
                                                                               ProLeuLeulleLeuGlyAsnGluHisMetThrAsnGlyGlnProSerCysSerValCys
                                                                                                                                                                                                  GIGCCGITIGICIACCGGAAGAICIACGAGGCGGCCAAGITICGTIICGGCCGCCGCCGC
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                                         CCGCTGCTCTTTGGCCCGGGCGAGGTGTGCGACGCTCGGCTCCAGCGCTCCCAGGTGAGC
                                                                                                                   CGGGAACCCTCCTATGCCGCCTTCTCCACCCGCGCGCCTTCCACCTGCCGCTTGGCGTG
                                                                                                                                                                                                                                                                                                                      ArgAlaGlnLysHisLeuGluThrAlaIleAsnGlySerAlaThrThrProGluLysLys
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                                                                                                                                          of an aplysia 5-HT receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98337861; PubMed=9671650;
Angers A., Storozhuk M.V., Duchaine T., Castellucci V.F.
DesGroseillers L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 08, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) G-protein-coupled 5-hydroxytryptamine receptor. 5-HTAP1.
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-----ProAlaGluProValAsnValLeuThrIleGln 110
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                                                                                                                   Pictrantonio P.V., Jagge C.L.;
Pictrantonio P.V., Jagge C.L.;

"Cloning of a serotonin receptor 5HT7-like cDNA from mosquito Aedes agypti Clophera: Culididae) excretory and respiratory systems.";

"Cloning of a serotonin receptor 5HT7-like cDNA from mosquito Aedes agypti Clophera: Culididae) excretory and respiratory systems.";

submitted (JAN-2001) to the BMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-ROTEIN COUPLED RECEPTORS.

BMBL; AR296125; AAG49292.1;

CO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001804; F:rroceptor activity; IEA.

GO; GO:0001804; F:rroceptor activity; IEA.

GO; GO:0001804; F:rroceptor activity; IEA.

GO; GO:0001804; F:rroceptor activity; IEA.

GO; GO:0001804; F:rroceptor activity; IEA.

GO; GO:0001804; F:rroceptor activity; IEA.

R PRINTS; PRO0021; Tem. Coupled receptor protein signalin. . .; IEA.

R PRINTS; PRO00237; GPRCRENDORSN.

R PRINTS; PRO00237; GPROTEIN RECEP FI 1; 1.

R PROSITE; PSSO0237; GPROTEIN RECEP FI 1; 1.

R PROSITE; PSSO0237; GPROTEIN RECEP FI 1; 1.

R PROSITE; PSSO0237; GPROTEIN RECEP FI 2; Transmembrane.

G-protein coupled receptor; Transmembrane.
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SerSerSerAlaSerValSerAlaThrAlaIleAlaThrSerLeuProAlaLeuValAsp
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes.
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    aegypti (Yellowfever mosquito)
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20.17%
                                                                                                      SEQUENCE FROM N.A.
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Best Local Similarity:
                                           Neoptera; Endopte
NCBL_TaxID=7159;
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Pred. No.:
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RINTS; PR00237; GPCRRHODOPSN. ROSITE; PS00237; G PROTEIN_RECE PROSTIE; PS50262; G PROTEIN_RECE PROTEIN coupled receptor; Rece EQUENCE 492 AA; 56261 MW; 2 ent Scores: 6.66e-21 No:: 433.50 t Similarity: 42.528 Match: 20.138	167 GTCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	317 SerCysThrAsnAlaMetThrSerThrArgValGluHisGlyGluThrAlaArgCysPro 336 890TCCTGG 895
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                                                 uLeuAlaSerProTyrProValGlnGluProArgSer 376
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                                                                                                                                            oAlaGlySerLysProAspSerHisValValGlnHis 356
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vity; IEA.
e receptor activity; IEA.
jled receptor protein signalin. . .; IEA.
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PAL MEMBRANE PROTEIN (BY SIMILARITY).
Y 1 OF G-PROTEIN COUPLED RECEPTORS.
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tarrhini, Hominidae, Gorilla.
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SP_F1_2; 1.
Sptor; Transmembrane.
)12335E0403F1B90 CRC64;
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annotation update)
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                                                                 1022 ATCTGGAAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTTCAACCCCCTGATT
                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                       a serotonin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the nematode C. elegans: a platform for clogy. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEAM; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
Transmembrane.
                                                                                                                     TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
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                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Serotonin receptor (Hypothetical protein).
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             CCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGT
                                                                                                                                                                                                                                                                                                                                                                         Olde B., McCombie R.W.;
"Molecular cloning and functional expression canorhabditis elegans.";
J. Mol. Neurosci. 0:0-0(1997).
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                                                                                                                                                                                                                             Created)
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
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"Direct Submission.";
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Submitted (SEP-1994)
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"The sequence of C. e
Submitted (OCT-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N2;
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161 TrpLeuIleGlyPheLeuIleSerIleProProMetLeuGlyTrpArgThrProGluAsp 180
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|ValArgGlnGlyAspAspGlyAlaAlaLeuGluValIleGluValHisArgValGlyAsn 300
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                                                                                                                                                                                                                                                                                                                    104 LeuglyGlnValThrCysAspLeuPheileAlaLeuAspVal------LeuCysCys 120
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                                                                                                       26 ThrGly11eSerAspValThrPheSerTyrGlnVal11eThrSerLeuLeuGlyThr
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221 AlaAlaArgPheArgIleArgLysThrValLysLysValGluLysThrGlyAlaAspThr
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|SerPheGluArgLysAsnGluArgAsnAlaGluAlaLysArgLysMetAlaLeuAlaArg
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                                                    ProglyGlnGlyAsnAsnThrThrSerProProAlaProPheGluThrGlyGlyAsnThr
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Kitano T., Kobayakawa H., Saitou N.;

Kitano T., Kobayakawa H., Saitou N.;

Kitano T., Kobayakawa H., Saitou N.;

Silver Project.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C.-:- SIMILARITY BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR GO; GO:000484291.1; - GAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001684; F:rebodopsin-like receptor activity; IEA.

GO; GO:0001684; F:rebodopsin-like receptor activity; IEA.

DR GO; GO:0001186; P:G-protein coupled receptor protein signalin. ..; IEA.

DR PRINTS; PRO0217; GPCRRHODOPSN.

DR PROSITS; PS02237; G PROTEIN RECEP FI 1; 1.

DR PROSITE; PS02262; G PROTEIN RECEP FI 2; 1.

R G-protein coupled receptor; Transmembrane.

SEQUENCE 422 AA; 46121 MW; C2CCC9803EBFRF9B CRC64;
                                                           ||| :::||| ::: ||| 375 CysHisMetProGluLeuGlyAlaIlelleAsnTrpLeuGlyTyrSerAsnSerLeu
                                                                                                                               1067 ITCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
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SEQUENCE FROM N.A.
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---MetAlaAlaLeuTyrGlnValLeuAsnLysTrpThrLeuGlyGlnValThrCysAsp 110
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|IleLeuCysTrpLeuProPhePheIleValAlaLeuValLeuProPheCysGluSerSer 374
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                                                                                                                                                                                   TTCACGGTCCTGGTGGTGACGCTGCTAGTGCTG-----CTGATCGCTGCCACTTTCCTG
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                                                                                                                                                                                                                                                                             73 TyrLeulleGlySerLeuAlaValThrAspLeuMetValSerValLeuVrlLeuPro---
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|FeuleuLeuMetLeuValLeuTyrGlyArgIlePheArgAlaAlaArgPheArgIleArg
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                                                                                                PheSerTyrGlnValIleThrSerLeuLeuLeuGlyThrLeuIlePheCysAlaValLeu
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168 SerIleProProMetLeuGlyTrpArgThrProGluAspArgSerAsnProAsnGluCys
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------AlaArgGluArgLysThrValLysThrLeuGlyIleIleMetGlyThrPhe
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141 ProlleAspTyrValAsnLysArgThrProArgArgAlaAlaAlaLeuileSerLeuThr 160
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| |||SerGlyIleSerAspValThrPheSerTyrGlnValIleThrSerLeuLeuLeuGlyThr
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              Euteleostomi;
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troglodytes (Chimpanzee).
uryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
halia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                     Kitano T., Kobayakawa H., Saitou N.;
"Silver Project.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity:
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Pred. No.:
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| GluArgLysThrValLysThrLeuGlyIleIleMetGlyThrPheIleLeuCysTrpLeu
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|ValArgGInGlyAspAspGlyAlaAlaLeuGluValIleGluValHisArqValGlyAsn
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| AlaAlaArgPheArglleArgLysThrValLysLysValGluLysThrGlyAlaAspThr
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   GTAAAGGAAGCACCTGATGAGGCTGAAGTG---GTGTTCACGGCACAT-----
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01-OCT-2000 (TrEMBLrel. 15,
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ProLeuProAlaSerSerGlnThrArgLeuSerGlnAlaAsnLeuSerAlaAlaPro--- 29
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| LysValValLeuVallleLeuLeuAlaLeuPheThrLeuAlaThrThrLeuSerAsnAla 68
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 390 AA; 43417 MW; 08EB9731C84E7474 CRC64;
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SerGlySerArgAsnTrpArgLeuGlyValGluSerLysAlaGlyGlyAlaLeuCysAla
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 181 ArgSerAspProAspAlaCysThrIleSerLysAspHisGlyTyrThrIleTyrSerThr
                                                                                                      GCGGCCAAGTTTCGTTTCGGCCGCCGCCGGAGAGCTGTGCTGCCGTTGCCGGCCACC---
                                                                                                                                      AlaAlaArgPheArgIle-----ArgLysThrValLysLysValGluLysThrGly
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Sus.
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Cetartiodactyla; Suina; Suidae;
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Eukaryota; Metazoa; Chordata; Cran Mammalia; Eutheria; Cetartiodactyling TaxID=9823;
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                                               --ATCGCTGCCACTTTCCTGTGGAACCTG 223
               ---GluValLeuGlnAlaLeu 34
                                                                     55 PhevalLeuThrThr1leLeuLeuThrLysLysLeuHisThrProAlaAsnTyrLeuIle 74
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                                                                       934
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                                   ---AspAla 297
                                                                                                       LeuLeuGluLysLysLysLeuMetAlaAlaArgGluArgLysAlaThrLysThrLeuGly 317
                                                                                                                                                                                                                                          338 ProlleCysLysAspAlaCysTrpPheHisLeuAlaIlePheAspPhePheThrTrpLeu 357
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                                                                                                                                                                                                                                                                                               GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCC
                                                                       GAGAGGCGAGCAGCCATGATGGTGGGA
                                                                                                                                        ATTICTGATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCTTCTGACGGAACTCATCAGC
                                                                                                                                                                                                          GCCTGCAGCCTGCCCCCCATCTGGAAAAGCATATTTCTGTGGCTT
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The FANTON Consortium,
The FANTON Consortium,
Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDRAs.";
Nature 420:563-573 (2002).
MGD; MGI:96276; Htrid.
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Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 374 AA, 41593 MW, 2FE947DF7DBEF14D CRC64;
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1119
67
150
53
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
                              SerProvalTyrValAsnGlnValLysValArgValSer
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423.50
47.81%
30.59%
19.66%
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148 ArgThrProArgArgArgAlaAlaAlaLeuIleSerLeuThrTrpLeuIleGlyPheLeuIle 167
                                                                                                               :::::: |||::::|||
168 SerIleProProMetLeuGlyTrpArgThrProGluAspArgSerAsnProAsnGluCys 187
                                                                                                                                                                                                                      355 IleLeuCysTrpLeuProPhePheIleValAlaLeuValLeuProPheCysGluSer8er 374
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| LeudanProvalIleTyrAlaTyrPheAsnLysAspPheGlnAsnAlaPheLysLysIle 414
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375 CysHisMetProGluLeuGlyAlaIleIleAsnTrpLeuGlyTyrSerAsnSerLeu
                                                                                                                                                                                        CAGGIGAGCCGCGAACCCTCTATGCCGCCTTCTCCACCCGCGCGCCCTTCCACCTGCCG
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                                                                                 GCCCTCGCGCCGCTCTTTGGCCGGGGGGGGTGTGCGACGCTCGGCTCCAGCGCTGC
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MGD; MGI:96273; Htrla.

GO; GO:0016021; Ciintegral to membrane; IEA.

GO; GO:0015824; F.rhodopsin-like receptor activity; IEA.

GO; GO:0001884; F.rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IRRO00276; GPCR Rhodops.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR00237; GPRCTEIN RECEP FI.; 1.

PROSITE; PS50262; GPRCTEIN RECEP FI.; 1.

PROSITE; PS50262; GPRCTEIN RECEP FI.; 1.

PROSITE; PS50262; GPRCTEIN RECEP FI.; 1.
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---MetAlaAlaLeuTyrGlnValLeuAsnLysTrpThrLeuGlyGlnValThrCysAsp 110
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                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Cortex, and Hippocampus;
STRAIN=C57BL/6J; TISSUE=Cortex, and Hippocampus;
The FANTOM Consortium.
The FANTOM Consortium Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs.";
Nature 420.563-573 (2002)
EMBL; AK043668; BAC31611.1;
EMBL; AK049814; BAC333931.1;
EMBL; AK049814; BAC33391.1;
EMBL; AK049814; BAC333970.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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116
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123
96
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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AspPheArgGlnAlaPheGlnLysVal 367
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01-0CT-2003 (TrEMBLrel. 25, Last
5-bydroxytryptamine 1A receptor.
HTR1A.
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423.00
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                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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900I DDB-----

us-09-976-782-15.n2p.rpr

OM nucleic

Run on:

Sequence:

receptor

receptor receptor receptor receptor receptor receptor

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A;Residues: 1-370 <RES>
A;Residues: BMBL:X69867; NID:g288735; PIDN:CAA49501.1; PID:g288736
C;Superfamily: octopamine receptor type I
C;Superfamily: octopamine receptor; glycoprotein; neurotransmitter receptor; transmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Datessaion: 148231
R;Matthes, H.; Boschert, U.; Amlaiky, N.; Grailhe, R.; Plassat, J.L.; Muscatelli, F.;
Mol. Pharmacol. 43, 313-319, 1993
A;Title: Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors define a new A;Reference number: 148231; MUID:93196607; PMID:8450829
                                                                                                                                             serotonin receptor
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alpha-2C-adrenergi
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Mismatches:
Indels:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-370 <RES>
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S58868
A47385
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A48881
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S26048
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A45121
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A31237
DYHUD2
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Percent Similarity:
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=Cggl2 1/USFTO spool p/US09976782/runat 31082004 115951 10328/app query.fasta_1.1351
-Q=Cggl2 1/USFTO spool p/US09976782/runat MINMATCH=0.1 -LOōPEXT=0 -LOODEXT=0
-UBNITS-EDITS 78 -QFMT=fastan -SUFFIX=h2ps -MINMATCH=0.1 -LOŌPEXT=0
-UNITS-EDITS -COOPEXT=1 -EMD=-1 -MATRIX=blosum62 - TRANS=human40.cdi -LIST=45
-UORTALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWHP=Ppto -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=200000000
-UOTFWHP=Ppto -NORM=ext -HEAPSIXE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976782 @CGN 1 1.64 @runat 31082004 115951 10328 -NCPD=6 -TCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(c) 1993 - 2004 Compugen Ltd.
                                                        protein search, using frame_plus_n2p model
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Maximum Match 100%
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length: 2000000000
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                            CTAGTGCTGCTGCTGCCACTTTCCTGTGGAACCTGCTTCCGGTCACCATCCCG 244
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LeulleLeubroGlyArgGluProProPheSerAlaPheThrValLeuValValThrLeu
                                                                  ceeerccereccrrccaccecereccecaraacrreereccrceacceccrrcaac
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Serotonin receptor 5B - rat
NiAlternate names: 5-hydroxytryptamine receptor 5B (5-HTR5B)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
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C; Accession: S38744; A47472

R; Wisden, W.; Parker, E.W.; Mahle, C.D.; Grisel, D.A.; Nowak, H.P.; Yocca, F.D.; Felder, FEBS Lett. 233, 25-31, 1993

A; Title: Cloning and characterization of the rat 5-HT(5B) receptor. Evidence that the 5-13 A; Accession: S38744

A; Accession: S38744

A; Reference number: S38744; MUID: 94039744; PMID: 8224165

A; Residues: 1-369 kMIS.

A; Residues: 1-369 kMIS.

A; Residues: 1-369 kMIS.

B; Rilander, M.G.; Lovenberg, T.W.; Baron, B.M.; de Lecea, L.; Danielson, P.E.; Racke, M. R; Residues: 1-369 kMIS.

A; Reference number: A47472

A; Reference number: A47472; MUID: 93234515; PMID: 7682702

A; Reference number: A47472

A; Reference number: A47472

A; Residues: preliminary

A; Molecule type: nucleic acid

A; Residues: 1-176, 1'177-369 kMID: 310074; PIDN: AA40616.1; PID: 9310075

A; Residues: 1-176, 1'177-369 kMID: 9324515; PMID: 940616.1; PID: 9310075

A; Residues: 1-176, 1'177-369 kMID: 94040616.1; PID: 9310075

A; Reperimental source: hypothalamus

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C; Superfamily: octopamine receptor: transmembrane protein

C; Reywords: G protein-coupled receptor; transmembrane protein
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Cindywords: a process compress ready as the contract of the co	don't more day		4
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	1.8e-87 1443.00 83.38% 78.10% 66.99%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	369 296 20 53 10
US-09-976-782-15 (1-1152) x S38744 (1-369)	52) x S38744	(1-369)	

-09-976-782	-15 (1-1152) x S38744 (1-369)
	5 ATGGAGGCGCTAGCCTTTCAGTGGCCACCGCGGGGTTGCCCTTGCCCTGGGGGGGG
9 7	65 ACCAGCAGCGGACCCCGAGCCCGAGGGGATACTCGGTTCGACCCCGAGCGGC 124 :::
12	125 GCCGTCCTGCCGGCCGAGGCCCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTG 184 :::
18	185 CTAGTGCTGCTGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG 244
24.	45 CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC 304
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36	365 CGTCGGCTGCTGGCGCGGAGCCTGTGCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424
4 H	425 CTGTGCTGCCCGCCGGCCTCGGGAACGTCGCGCCATCGCCCTGGGCCGCGACGGGGCC 484
11 4	485 ATCACACGCACCTGCAGCACACGCTCCCAGCCGCGCGCGC
ry in	545 GCGCTCGCCCGGGGTGCCGTCGCGCTCCGCGCCGCTGCTCTTTGGCCGGGGC 604
9	605 GAGGIGIGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 664

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Db 195 GlualaryrAspalaArgLeuGlnArgCysGlnValSerGlnGluProSerTyrAlaVal 214 Oy 665 TICTCCACCGGGGGCCTTCCACGGGGGTGGTGGTGTTACGGAAG 724	215	Db 235 IleTyrLysAlaAlaLysPhedlyArgArgArgArgAlaValbroLeuPro 254 Qy 785 GCCACCATGCAGGTCCAAGGTAAAGAAGCACCTGAAGAGGCTGAAGTGGTTC 844	29	Qy 905 AAGGAGAGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGG 964	Oy 965 AICCCCTTCTTCCTGACGGAACTCAICAGCCCACTCTGTGCCTGCAGCCTGCCCCCCAIC 1024	Qy 1025 TGGAAAAGCATATTCTGTGGCTTGGCTACTCCAATTCTTCTTCACCCCTGATTTAC 1084	Qy 1085 ACAGCTITIAACAAGAACTACAACAACAATGCCTTCAAGAGCCTCTTTACTAAGAGAGA 1141 DD 351 ThrAlaPheAsnLysAsnLyrAsnAsnAlaPheLysSerLeuPheThrLysGlnArg 369	RESULT 3 137107 5-HT5A serotonin receptor - human C;Species: Homo sapiens (man) C;Date: 29-Mav-1998 #secuence revision 29-Mav-1998 #text change 21-Th1-2000	, Kilpatric	e number: 137107; MUID:95080386; PMID:7988681 137107; translated from GB/EMBL/DDBJ type: DNA	A;Residues: 1-357 <res> A;Cross-references: EMBL:X81411; NID:g541776; PIDN:CAA57168.1; PID:g784990 C;Genetics: A;Gene: 5-HT5A</res>	A,Introns: 247/3 C,Superfamily: octopamine receptor type I Alignment Scores:		1: 49.37% Indels: 2 Gaps: Gaps: 782-15 (1-1152) x 137107 (1-347)	CARCAGCGGACCCGGGACC SerbheSerLeuSerThr CGTCCTGCCGGGCCGAGGG ::

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C.Species: M.G.; Lovenberg, T.W.; Baron, B.W.; de Lecea, L.; Danielson, P.E.; Racke, M. Proc. Natl. Acad. Sci. U.S.A. 90, 3452-3456, 1993
A;Title: Two members of a distinct subfamily of 5-hydroxytryptamine receptors differenti
A;Reference number: A47472; MUID:9324515; PMID:7682702
A;Status: preliminary
A;Nolecule type: nucleic acid
A;Residues: 1-357 < CRL>
A;Residues: 1-357 < CRL>
A;Residues: 1-357 < CRL>
A;Residues: sequence extracted from NCBI backbone (NCBIN:129674, NCBIP:129677)
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; transmembrane protein
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	Db 128 SerileTroAsnValhrAlalleAlaLeussoArdTvrTroSerileThrArdisLeu	500 CAGCACACGCGCACCCGCAGCCGGCCTCGTTGCTCATGATCGCCGCTCGCCCGGGTG	Db 148 GluTyrThrLeuArgAlaArgLysArgValSerAsnValMetIleLeuLeuThrTrpAla 167	Qy 560 CGGTCGGCGCTCATCGCCCTCGCGCCGCTGCTTTTGGCCGGGGCGAGGTGTGCGACGCT 619	CGGCTCCAGCGCTGCCAGGTGAGCCGGAACCCTCTATGCCGCCTTCTCCACCCGCGGC :::	GCGGCC AlaAla		Qy 797 GTGAGGTCCAAGGAAAGGAACCCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGC 856	Oy 857 AAAGCAACGGTGTCCTTCCAGGTGAGCGGGACTCCTGGCGGGAGCAAAGGAGGGGGA 916	Qy 917 GCAGCCATGATGGTGGAATTCTGATTTGTGCTGTGTTGTGCTGGATCCCCTTCTTC 976	Qy 977 CTGACGGAACTCATCAGCCCACTCTGTGCCTGCGCCTGCCCCCCATCTGGAAAAGCATA 1036 :::	Oy 1037 THTCTGTGGCTTGCTACTCCAATTCTTCTAACCCCCTGATTTACACGCTTTTAAC 1096	Oy 1097 AAGAACTACAACATGCCTTCAAGAGCCTCTTTACTAAGGAGAGA 1141 ::::: ::::	RESULT 6 S68422 serotonin receptor 1D beta - rabbit N:Alternate names: 5-hvdroxvtrvotamine receptor 1D beta (5-HTR1Dheta)	C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999 C;Accession: S68422	<pre>A.harwood, G.; Lockyer, M.; Giles, H.; Fairweather, N. FEBS Lett. 377, 73-76, 1995 A.Title: Cloning and characterisation of the rabbit 5-HT(1D-alpha) and 5-HT(1D-beta) rec A.Reference number: S68422; MUID:96130324; PMID:8543023</pre>		A;Cross-reterences: EMBL:Z50163; NID:gl004283; PIDN:CAA90531.1; PID:gl004284 C;Superfamily: vertebrate rhodopsin C;Keywords: neurotransmitter receptor	Length: Matches:	Similarity: 51.59% ocal Similarity: 34.20% fatch:	

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A;Map position: 6q14.3-6q16.3

C;Superfamally: vertebrate rhodopsin

C;Superfamally: vertebrate rhodopsin

C;Superfamally: vertebrate rhodopsin

C;Superfamally: vertebrate rhodopsin

C;Superfamally: vertebrate rhodopsin

C;Superfamally: vertebrate rhodopsin

C;Superfamally: vertebrate status predicted <TM1>
F;84-112/Domain: transmembrane #status predicted <TM2>
F;124-145/Domain: transmembrane #status predicted <TM4>
F;126-129/Domain: transmembrane #status predicted <TM4>
F;166-129/Domain: transmembrane #status predicted <TM4>
F;167-129/Domain: transmembrane #status predicted <TM6>
F;167-129/Domain: transmembrane #status predicted <TM7>
F;24,32/Binding site: phosphate (Ann) (covalent) #status predicted
F;252,313/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict F;388/Binding site: phosphate (Thr) (covalent) Hstatus predicted
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| 102 ValMetPro-----IleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGIn 119
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-------TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGAGACCAGCAGCGCGGGACCCCGAAGCCCCGAGAGGGATACTCGGTTCGACCCCG
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                                                                                                                                                                                                                    Neternate names: 5-hydroxytryptamine 1D receptor beta; 5-hydroxytryptamine receptor 1B Selection and Selection of Alternate names: 5-hydroxytryptamine 1D receptor beta; 5-hydroxytryptamine receptor 1C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo Sapiens Selection C; Species: John Carlot C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; John C; Species: John C; Species: John C; Species: John C; Species: John C; Species: John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; John C; J
                                                                                                                                                                                                serotonin receptor 1B - human
N'Alternate names: 5-hydroxytryptamine 1D receptor beta; 5-hydroxytryptamine receptor
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A;Title: Characterization of the human 5-hydroxytryptamine-1B receptor.
A;Reference number: A42146; WUID:92210526; PMID:1348246
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108 407 128 467 145 527 165	Oy 587 CTGCTCTTTGGCCGGGCGAGGTGTGGGCTCGGCTGCCAGGTGAGCCGG 646 Db 185PhePheTrpArgGlnAlaLysAlaGluGluValSerGluCysLeuValAsnThr 203 Oy 647 GAACCTCCTATGCCGCTTCTCCACCCGGGCGCTTCGCGCTTGGGTG 703 :::	Oy 779 TTGCCGCCCCATGCAGGTCCAAGGTAAAGGAACCCCTGATGAGGTCCGAA 835 Db 264 ThrThrSerValThrSerIi=sniberkrgalaProispyalproderTuber129sr 283 Oy 836 GTGGTGTTCACGCCACATTGCAAACCAACGGTGCCTCCAGGTGAGCTCTGG 895 Db 284 ProValTyrValAsnGlnValLysValArgValSerAsphalatu 298 Oy 886 GGGGAGCAAGG
Qy 740 AAGTTTCGTTTC	0y 914 CGAGCACCATGATGGTGGAATTCTGATTGGGTGTTTGTGCTGCTGCTCCCTTC 973 11 LysAlaThrLysThrLeuGly1le1leLeuGlyAlaPheIleValCysTrpLeuProPhe 330 Qy 974 TTCCTGAGGAACTCATCAGCCACTCTGTGCCTGCACCCCCATCTGG 1027	REBULT 8 Serotomin receptor 1-like - rabbit C. Serotomin receptor 1-like (5-HTR) C. Species: Oryctolagus cuniculus (domestic rabbit) C. Date: 11-J01-1996 #sequence_revision 01-Mar-1956 #text_change 05-Nov-1999 C. Date: 10-J01-1996 #sequence_revision 01-Mar-1956 #text_change 05-Nov-1999 R. Wurch. A. Accession: S69126 A. Accession: S69126 C. Negwords: 10-J01-1996 #text_change 05-Nov-1999 C. Superfamily: vertebrate rhodopsin C. Negwords: 10-J01-1996 #text_change 05-Nov-1999 C. Superfamily: vertebrate rhodopsin C. Superfamily: vertebrate r

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Serotonin receptor 1B - Chinese hamster
NiAlternate names: 5-hydroxytryptamine receptor 1B (5-HTR1B)
C;Species: Cricetulus griseus (Chinese hamster)
C;Decies: Cricetulus griseus (Chinese hamster)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S54153
E;Murch, T.; Palmier, C.; Colpaert, F.C.; Pauwels, P.J.
Submitted to the EMBL Data Library, April 1995
A;Description: Molecular cloning and expression of a Chinese hamster lung fibroblast CDN
A;Reference number: S54153
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275 AsnHisValGlnValLysLeuAla-----GluGlyValLeuGluArgLysArgIle 291
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-386 <WUR>
A,Cross-references: BMBL:X86458; NID:g790985; PIDN:CAA60175.1; PID:g790986
C,Superfamily: vertebrate rhodopsin
C,Keywords: neurotransmitter receptor
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A,Cross-references: EWBL:X14049; NID:9900; PIDN:CAA32207.1; PID:9901
R,Libert, F.; Parmentier, M.; Lefort, A.; Dumont, J.B.; Vassart, G.
Nucleic Acids Res. 18, 1916, 1990
A,Title: Complete nucleotide sequence of a putative G protein coupled recept
A,Reference number: S12822; MUID:90245610; PMID:2159630
A,Accession: S12822
A,Actatus: translation not shown
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-377 <LI2>
A,Cross-references: EMBL:X14049; NID:9900; PIDN:CAA32207.1; PID:9901
C,Genetics:
C,Genetics:
C,Genetics:
C,Superfamily: octopamine receptor type I
C,Superfamily: octopamine receptor; glycoprotein; transmembrane protein
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herAlaAspGlyTyrIleTyrGlnAspSerIleAlaLeuPro--- 43
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om NCBI backbone (NCBIN:93807, NCBIP:93808)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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C;Species: Drosophila melanogaster C;Accession. A38271 R;Witz, P.; Amlaiky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R. R;Witz, P.; Amlaiky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R. Proc. Natl. Acad. Sci. U.S.A. 87, 8940-8944, 1990 A;Title: Cloning and characterization of a Drosophila serotonin receptor that activates A;Reference number: A38271, MUID:91062395; PMID:2174167 A;Accession: A38271, MUID:91062395; PMID:2174167 A;Accession: A38271, MUID:91062395; PMID:2174167 A;Accession: B38271, MUID:91062395; PMID:2174167 A;Accession: B185533 A;Accession: B185533 A;Gree: the authors translated the codon CTT for residue 213 as Ala, GTG for residue 215 C;Genetics: A;Gene: FlyBase:5-HT7 A;Cross-references: RlyBase:FBG00004573 C;Guperfamily: octopamine receptor type I C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein; phosphoprotein	298 644 318 704 764 351
Alignment Scores: Pred. No.: Score: Score: 435.50 Matches: Percent Similarity: 45.15\$ Conservative: Best Local Similarity: 20.22\$ Mismatches: 20.22\$ Gaps: 12	371 GlySerProSerAlaProGlnAlaProProLeuGlyHisThrGluLeuAlaSerSerG 809 GTAAAGGA
US-09-976-782-15 (1-1152) x A38271 (1-564) QY	410 lyLeuSerSerGlyGlyGlyAlaLeuAlaGlyHisGlySerGlyGlyGlyValSerGlyS 881 AGCGGGGACTCCTGCCGGGA
74 GGACCCGGGACC	OY 1 AGGGGACCAGCAGGGGGGGAATTGGCGTTTGTGTTGTGT
ON 123 GINGLYLLEININSETINIASDLEUGLYASPSERASNINFINFLEUVALPFOLEUSERASP 142 QY 146 CCGCCCTTC	Oy 1031 AGCATATTTCTGTGGCTTGGCTACTCCAATTCTTTCTACCCCCTGATTTACACAGCT 1090 :::
	Qy 1091 TTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126 : : : : : : : : : : : : : : :
227 GTTCCGGTCACCATCCCGGGGTCCGTGCCTTCCACCGCGTGCCGATAACTTGGTGGCC 286	RESULT 14 T42203 serotonin receptor 5-HT precursor - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 R;Olde, B.; McComble, W.R.
222 406 240	J. Mol. Neurosci. 8, 53-62, 1997 A;Title: Molecular cloning and functional expression of a serotonin receptor from Caenority. A;Reference number: Z22071; MUID:97215250; PMID:9061615 A;Reference number: Z22071; MUID:97215250; PMID:9061615 A;Accession: T42203 A;Accession: T42203 A;Accession: T42203 A;Accession: T42203 A;Accession: T42203 A;Accession: T42203
466 257 526	A,Residues: 1-4f5 <0LD). A,Residues: 1-4f5 <0LD). A,Cross-references: EMBL:U15167; PIDN:AAB66360.1 A,Experimental source: clone CER-1 C,Superfamily: vertebrate rhodopsin C;Keywords: transmembrane protein
Db 258 ValAepArgTyrLeuAlaileThriysProleuGiuTyrGlyValLysArgThrProArg 277 Qy 527 GCCTCGTTGCTGCTCGCCCGGGGTGCCCTCGGCCCTCGCGCG 586 :::	Alignment Scores: 7.14e-21 Length: 445 Pred. No.: 431.50 Matches: 135 Score: 431.50 Matches: 61 Percent Similarity: 44.24 Conservative: 61 Percent Similarity: 30.47\$ Mismatches: 156 Query Match: 20.03\$ Indels: 13 Base Local Similarity: 20.03\$ Caps: 13

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A;Map position: 1p36.3-1p34.3
A;Introns: #status abbeat
C;Superfamily: octopamine rece
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A; Molecule type: mRNA
A; Residues: 1-377 < WEI>
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                                                                                     22 SerAlaValAlaArgĠİYThrHisLeuValAspGlnPheProAlaHisAlaGluIlePhe
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                      CTTGCCCTTGGGACCCGAGACCAGCAGCGGACCCCGAGACCCCGAGAGGGGATACTC
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US-09-976-782-15 (1-1152) x T42203 (1-445)
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Section receptor 1D - human
N.Alternate names: 5-hydroxytryptamine receptor 1D (5-HTR1D); 5HT-1D alpha receptor
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: A53279; A44136
R; Hamblin, M.W.; Metcalf, M.A.
Mol. Pharmacol. 40, 143-148, 1991
A; Pitle: Primary structure and functional characterization of a human 5-HT-1D-type serot
A; Reference number: A53279; MUD: 91342595; PMID: 1652050
A; Molecule type: DNA
A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM>A; Residues: 1-377 < HAM
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R;Weinshank, R.L.; Zgombick, J.M.; Macchi, M.J.; Branchek, T.A.; Hartig, P.R.
Proc. Natl. Acad. Sci. US:A. 89, 3630-3634, 1995
A;Title: Human serotonin ID receptor is encoded by a subfamily of two distinct genes: 5-A;Reference number: A44136; MUID:92228840; PMID:1565658
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C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
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                                                                                                                                                                                   376 ThrPheValAlaCysTrpThrProPhePheLeuValSerIleTyrArgProIleCysGly
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941 ATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTC 1000
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   ----AlaThrValLeuSerAsnAla
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APPLICANT: Grosse et al

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-LOBPLIShed_Applications AA -QFMT=fastan -SUPFIX=app.xapb - MINAPGH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosume6
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN-0 -ALIGN=15 -MODE=LOAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09976782 @CGN 1 1 225 @runat 31082004 115953 10443
-NCPU=6 -IGPU=3 -NO MMAP -LARGEQUERY -NEG $$GORES = NAIT -DSPBLOGR=100
-LONGLGG -DEV TIMEOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-LOADGLOG -DEV TIMEOUT=30 -YGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                    August 31, 2004, 20:21:44; Search time 160 Seconds (without alignments) 4530.426 Million cell updates/sec
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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US-10-333-946-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B. APPLICANT: ARVIZU, Chandra S.; IAL, Preeti G.; APPLICANT: BURFORD, Nell; YUB. Henry APPLICANT: BURFORD, Nell; YUB. Henry APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.; APPLICANT: RALICK, Deborah A.; CHAMLA, Narinder K.; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam, APPLICANT: GRAUL, RICHART C.; WARREN, Bridget A.; APPLICANT: GRAUL, RICHART C.; WARREN, Bridget A.; APPLICANT: LEE, Ernestine A.; DING, Li
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CURRENT APPLICATION NUMBER: US/10/33,946
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US/10/3433
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-27
PRIOR PLING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/223,268
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-09-13
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Sequence 15, Application US/10333946
Publication No. US20040023252A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-10-16
PRIOR PILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 127
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                                                                                   GENEKAL INFORMATION:

GENEKAL INFORMATION:

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APPLICANT: Spytek, Rimberly
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TILLE REPERENCE: 15966-745
TILLE REPERENCE: 15966-745
TILLE REPERENCE: 15966-745
TILLE REPERENCE: 15966-745
CURRENT APPLICATION NUMBER: 60/193,339
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ORGANISM: Homo sapiens
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APPLICANT: WALSO, ROWELLY,
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APPLICANT: THORNYON, Michael B.
APPLICANT: THORNYON, Michael B.
APPLICANT: THORNYON, Michael B.
TILLE OF INVENTION G-PROTEIN COUPLED RECEPTORS
FILE REPRENCE: PI-0131 USN
CURRENT APPLICATION NUMBER: US/10/311,671
CURRENT APPLICATION NUMBER: PCT/USO1/19275
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PRIOR FILING DATE: 2000-06-20
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PRIOR FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-07-14
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NAME/KEY: misc_feature
OTHER INFORMATION: 1ncyte ID No: 7474977CD1
                                                             LU, Dyung Aina M.
TRIBOULEY, Catherine
                                                                                                                                                     YANG, Junming
RAMKUMAR, Jayalaxmi
AU-YOUNG, Janice K.
ELLIOTT, Vicki S.
                                                                                                                                                                                                         ELLIOTT, VICKI S.
HERNANDEZ, RODETCO
WALSH, ROGETICK T.
BOROWSKY, Mark L.
THORNTON, Michael B.
                                                                                           LU, Yan
CHAWLA, Narinder K.
GRAUL, Richard
YAO, Monique G.
                              KHAN, Farrah A.
ARVIZU, Chandra S.
GRIFFIN, Jennifer
               YUE, Henry
KHAN, Farra
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ORGANISM: Homo sapiens
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Sequence 8, Application US/10311671
Publication No. US20040072996A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti G.
APPLICANT: HAPALIA, April J. A.
APPLICANT: HAPALIA, April J. A.
APPLICANT: GANDHI, Amene B.
APPLICANT: KALLICK, Deborah A.

US-10-311-671-8

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APPLICANT: TELERREY, VELLER AFT.
APPLICANT: MAINARKE, VELLER AFT.
APPLICANT: MAINARKE, VELLER AFT.
APPLICANT: MACONGELLE APPLICANT: GERLACH: VAREIE L.
APPLICANT: GERLACH: VAREIE L.
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APPLICANT: GERLACH: JOHN WERE: G./26.78
PRIOR APPLICANTION NURBER: G./26.79
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                    TCHERNEV, VELIZAR T
MALYANKAR, URIEL M.
SHENOY, SURESH
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ORGANISM: Unknown Organism
   GORMAN, LINDA
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LENGTH: 38(
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JUS-09-564-342-30

Sequence 30, Application US/09954342

Publication No. US20030170838A1

GENERAL INFORMATION:
APPLICANT: MISHRA, VISHNU S.
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: VERNET, CORINE A.
APPLICANT: VERNET, CORINE A.
APPLICANT: COLMAN, STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785
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; OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide US-09-954-342-30
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FUBLICANT: GENERAL INFORMATION:
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gusev, Vladimir Y
APPLICANT: Burgees, Catherine
APPLICANT: Burgees, Kunud
APPLICANT: Majumder, Kunud
APPLICANT: Patturajan, Meera
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
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APPLICANT: Padigaru, Muralidhar
APPLICANT: Saturajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderra, Steven K
APPLICANT: Spaderra, Steven K
APPLICANT: Spaderra, Steven K
APPLICANT: Spaderra, Steven K
APPLICANT: Taubier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: 06/193,339
RRIOR PILING DATE: 2001-03-29
RRIOR PILING DATE: 2000-03-30
RRIOR PILING DATE: 2000-04-05
RRIOR PILING DATE: 2000-04-05
RRIOR PELING DATE: 2000-04-05
RRIOR APPLICATION NUMBER: 60/195,388
RRIOR APPLICATION NUMBER: 60/195,088
RRIOR APPLICATION NUMBER: 60/195,088
RRIOR RILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-10
PRIOR PELING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR PILING DATE: 2000-04-14
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ORGANISM: Rattus norvegicus
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Best Local Similarity:
Query Match:
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LENGIH: 370
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US-09-976-782-15 (1-1152) x US-09-823-187-57 (1-370)
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Sequence 57, Application US/09823187 Publication No. US20030096952A1 GENERAL INFORMATION:

-09-823-187-57

APPLICANT: Burgess, Catherine APPLICANT: Gusev, Vladimir Y APPLICANT: Liu, Xiaohong APPLICANT: Majumder, Kumud

Length:
Matches:
Conservative:
Mismatches:
Indels:

4.04e-82 1453.50 83.38% 78.10% 67.48%

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65 ACCAGCAGCGGACCCGGGACCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGCGGC 124
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                                                                                       THEREBY
                                               APPLICANT: EASTELL, LUCA

TITLE OF INVENTION: NOVEL POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THERE
FILE REFERENCE: 2.1402-14
CURRENT PILING DATE: 2001-09-17
FRICH REPLICATION NUMBER: 60/233,382
FRICH APPLICATION NUMBER: 60/240,498
FRICH APPLICATION NUMBER: 60/260,284
FRICH APPLICATION NUMBER: 60/260,284
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FRICH RILING DATE: 2000-01-13
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FRICH RILING DATE: 2001-01-29
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LENGTH: 370
TYPE: PRT
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                                                           CTGTGCTGCCCCGCCGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGGGCC 484
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              ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal----
Sequence 56, Application US/09954342
Publication No. US20030170838A1
GENERAL INFORMATION:
APPLICANT: MISHRA, VISHUN S.
APPLICANT: SPYTEK, KIMBERLY ANN
APPLICANT: VENDET, CORINE A.
APPLICANT: VENDET, CORINE A.
APPLICANT: OCLAMAN, STEVEN D.
APPLICANT: GOLMAN, STEVEN D.
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MALYANKAR, URIEL M.
SHENOY, SURESH
PADIGARU, MURALIDHARA
GERLACH, VALERIE I.
MACDOUGALL, JOHN R.
SMITHSON, GLENNDA
MILLET, ISABELLE
BEYMAN, JOHN
STONE, DAVID
GUNTHER, ERIK
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PRIOR APPLICATION NUMBER: 60/240,732
PRIOR FILING DATE: 2000-10-16
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PRIOR PILING DATE: 2000-10-16
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Sequence 101, Application US/09976782
Publication No. US20030190715A1
CENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: NO. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-157
CURRENT APPLICATION NUMBER: US/09/976,782
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/240,113
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-16
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Mismatches:
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APPLICANT: Spaderna, Richard A
APPLICANT: Spaderna, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/0993,187
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
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PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 2000-04-10
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Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
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APPLICATION WUMBER: 60/197,081
FILING DATE: 2000-04-13
APPLICATION NUMBER: 60/197,525
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PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/233,960
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/233,402
PRIOR FILING DATE: 2000-09-18
PRIOR PRILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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Query Match:
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APPLICANT: EASTELLI, LUCA
APPLICANT: ZERHUSEN, BRYAN
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-114
CURRENT APPLICATION NUMBER: US/09/954,342
CURRENT PILING DATE: 2001-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-10-13
FRIOR FILING DATE: 2000-10-13
FRIOR FILING DATE: 2000-10-13
FRIOR PELICATION NUMBER: 60/260,284
FRIOR FILING DATE: 2001-01-08
FRIOR PELING DATE: 2001-01-08
FRIOR PELING DATE: 2001-01-08
FRIOR APPLICATION NUMBER: 60/260,973
FRIOR APPLICATION NUMBER: 60/260,973
FRIOR APPLICATION NUMBER: 60/24,794
FRIOR APPLICATION NUMBER: 60/232,675
FRIOR PELING DATE: 2000-10-06
FRIOR FILING DATE: 2000-09-15
FRIOR PELING DATE: 2000-09-15
FRIOR PELING DATE: 2000-09-15
FRIOR APPLICATION NUMBER: 60/233,801
FRIOR APPLICATION NUMBER: 60/233,801
FRIOR APPLICATION NUMBER: 60/233,801
FRIOR APPLICATION NUMBER: 60/233,676
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                                AAGGAGAGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGTGCTGG 964
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            GCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTC
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APPLICANT: SPYTEK, KIMBERLY ANN
APPLICANT: SPYTEK, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: OCOLMAN, STEVEN D.
APPLICANT: GORMAN, INDA
APPLICANT: GORMAN, STEVEN D.
APPLICANT: TCHERNEY, VELIZAR T.
APPLICANT: GRENACR, URLIZAR T.
APPLICANT: GERLACH, VALERIE I.
APPLICANT: GRIACH, VALERIE I.
APPLICANT: MALVANKAR, URIEL I.
APPLICANT: SMITHSON, GIERNDA
APPLICANT: SMITHSON, JOHN R.
APPLICANT: STONE, DAVID
APPLICANT: STONE, DAVID
APPLICANT: GUNTHER, ERIK
APPLICANT: GUNTHER, ERIK
APPLICANT: GUNTHER, ERIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/09954342 Publication No. US20030170838A1 GENERAL INFORMATION:
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RASTELLI, LUCA
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| ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal-----
370
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                                   Conservative:
Mismatches:
Indels:
                                                                                                                         US-09-976-782-15 (1-1152) x US-09-954-342-57 (1-370)
 Length:
Matches:
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124 38

Percent Similarity: 83.64% Conservative: 19 Best Local Similarity: 78.63% Mismatches: 53 Query Match: 67.43% Indels: 9	10 Gaps: -976-782-15 (1-1152) x US-09-976-782-102 (1-370)	Qy 5 AIGGAGGCGGTAGCCTTTCAGTGGCCACGGCGGGTTGCCCTTGCCCTGGGAG 64	Qy 65 ACCAGCAGCAGCCGAACCCCAAGCCCGAGAGGATACTCGGTTCGACCCCGAGCGGC 124 ::	OY 125 GCCGTCCTGCCGGCCGCCGCTTCTCTCTCTCACGGTCCTGGTGGTGGTGGTGG 184 :::	QY 185 CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGGTGGTTCCGGTCACCATCCCG 244	Qy 245 CGGGTCCGTGCCTTCCACCGCGTGCCGATAACTTGGTGGCCTCGACGGCCGTCTCGGAC 304	Qy 305 GAACTAGTGGCAGCTGGCATGCCAGCCGAGCCTGGCGAGTGACCTGTCGACCGGGGGA 364	Qy 365 CGTCGGCTGCTGGCCACCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424	Qy 485 AICACACGCACCIGCAGCACACGCACCCGCACCGCGCCTCGTIGCTCATGATC 544	61 60	605 GAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 66	196 GlualaTyraspalaArgLeuGlnArgCysGlnValSerGlnGluProSerTyrAlaVal 21 665 TTCTCCACCGCGGGGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG 72	Db 216 PheSerThrCysGlyAlaPheTyrLeuProLeuAlaValLeuPheValTyrTrpLys 235 Qy 725 ATCTACGAGGCGCCAAGTTTCGTTTCGGCCGCCGCCGCAGAGCTGTGCCGTTGCCG 784	Db 236	Qy 785 GCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTC 844	845 ACGCACATIGCAAAGCAACGIGICCTICCAGGIGAGCGGGGACTCCTGGCGGAGCAG	Db 272 ThralaargargargatathrValThrPheGlnThrSerGlyAspSerTrpargGluGln 291 Qy 905 AAGGAGGGAGCAGCCATGATGATGGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGG 964	Db 292 LysGluLysArgAlaAlaMetMetValGly1leLeulleGlyValPheValLeuCysTrp 311	OY 965 ATCCCCTTCTTCCTGACGGAACTCACCCCCCTCTGTGCTGCTGCTGCCTGC
Oy 665 TICTCCACCGGGGGCCTTCCACCTGCCGTGGCGTGGTGCCGTTTGTCTACCGGAAG 724	Qy 725 ATCTACGAGGCGCCAAGTTTCGTTTCGGCCGCCGGGAAGCTGTGCTGCCGTTGCCG 784 Db 236 IleTvrtovsAlaAlatusPhadrcPhadrcAhadraLanarahadalanalanalanalanalanalanalanalanalanal	785 GCCACCATGCAGGTCCAAGGTAAAGCAACCACTGATGAGTGAG			CCCCCAIC		141		 TIED REFERENCE: 21402-157 CURRENT APPLICATION NUMBER: US/09/976,782 CURRENT FILING DATE: 2001-10-12	PRIOR APPLICATION NUMBER: 60/240,113 PRIOR FILING DATE: 2000-10-12 PRIOR APPLICATION NUMBER: 60/240,662 PRIOR FILING DATE: 2000-10-16	PRIOR APPLICATION NUMBER: 60/240,732 PRIOR FILING DATE: 2000-10-16 PRIOR FILING NAMBER: 60/240,625	FRIOR FILLING JATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/240,703 PRIOR FILLING DATE: 2000-10-16 PRIOR PRILING DATE: 2000-10-16 PRIOR PRILING NUMBER: 60/241,190	FALON FILLING DAILS: 2000-10-16 PRIOR FILLING DAILS: 2000-10-16 PRIOR PILLING DAILS: 2000-10-16 PRIOR APPLICATION NUMBER: 60/240,669	PRIOR FILING DATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/262,455	PRIOR FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: 60/240,648 PRIOR FILING DATE: 2000-10-16	NOWBER OF SEQ 1D NOS: 12/ SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 102 IBNGTH: 370	TYPE: PRT ; ORGANISM: Mus musculus	ignment Scores:	Pred. No.: 4.66e-82 Length: 370 Score: 1452.50 Matches: 298

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| AlaileThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly 195
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LAICANT: Patturajan, Meera

APPLICANT: Shimkets, Richard A

APPLICANT: Spacera, Steven K

APPLICANT: Spacera, Steven K

APPLICANT: Taupier, Raymond J

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745

CURRENT APPLICATION NUMBER: US/09/823,187

CURRENT APPLICATION NUMBER: 60/193,339

PRIOR FILING DATE: 2000-03-30

PRIOR PLING DATE: 2000-03-30

PRIOR PLING DATE: 2000-03-30

PRIOR PLING DATE: 2000-03-30

PRIOR PLING DATE: 2000-03-30

PRIOR PLING DATE: 2000-03-30

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PRIOR FILING DATE: 2000-03-30

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PRIOR FILING DATE: 2000-03-30
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. Sequence 59, Application US/09823187
. Publication No. US20030096952A1
. GENERAL INFORMATION:
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publication No. US2030009780A1

GENERAL INPORMATION:
APPLICANT: Allan.
FILE OF INVENTION: TRANSGENIC MICE CONTAINING 5-HT5B

TITLE OF INVENTION: TRANSGENIC MICE CONTAINING 5-HT5B

TITLE OF INVENTION: SEROTONIN RECEPTOR GENE DISRUPTIONS
FILE REPERENCE: R-601

CURRENT APPLICATION NUMBER: US/10/109,532A

CURRENT FILING DATE: 2002-03-28

PRIOR FILING DATE: 2001-03-29

PRIOR FILING DATE: 2001-03-29

PRIOR FILING DATE: 2001-12-21
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Matches:
Conservative:
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Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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Pred. No.:
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| 176 AlaThrTrpAlaLeu---SerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly 194
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|119 ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal-----
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Matches:
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-14
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ORGANISM: Rattus norvegicus
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                                                                                                                                                               904
                                                                                                                                                                                                                                           310
  724
                                                                                                                                                                          964
                                                                                                                                                                                                                                                                                                                                                                            ACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
             215 PheSerThrCysGlyAlaPheTyrValProLeuAlaValValLeuPheValTyrTrDLys
                                                  ATCTACGAGGCGGCCAAGTTTCGGTTTCGGCCGCCGGAGAGCTGTGCTGCCGTTGCCCG
                                                                 ACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG
TTCTCCACCGCGCGCCCTTCCACCTGCCGCTTGGCGTGCCGTTTTGTCTACCGGAAG
                                                                                                       GCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTC
                                                                                                                                                                                                                            291 LysGluLysArgAlaAlaMetMetValGlylleLeuileGlyValPheValLeuCysTrp
                                                                                                                                                                                                                 AAGGAGAGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGTGCTGG
                                                                              235
                                                                                                                                                             845
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665
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Search completed: August 31, 2004, 20:46:12 Job time : 184 secs